APPENDIX I

PROGRAM IDENTITY

```
Option Explicit
Dim FileName As String
Dim SaveFile As String
Dim filetmp() As String

Private Sub CmdMain_Click()

Dim Identity As Integer
Dim NumLoci As Integer
Dim Diff As Integer
Dim MisMatch As Integer
Dim NumSamp As Integer
Dim Ct As Integer
Dim Loc As Integer
Dim No As Integer
Dim Yes As Integer
Dim Fld As String
Dim LineNum As Integer
Dim LineNumA As Integer
Dim LineNumB As Integer
Dim LineStr As String
Dim I As Integer
Dim Identfld As Integer
Dim Samefld As Integer
Dim Maybefld As Integer
Dim ErrorCode As String
Dim lp As Integer
Dim lp2 As Integer
Dim DiffLoc As String
Dim B(500, 24) As String
Dim Temp() As String

Identity = Val(IdentityBox.Text)
MisMatch = Val(MisMatchBox.Text)
NumLoci = Val(NumLociBox.Text)
NumSamp = Val(NumSampBox.Text)

Identfld = NumLoci + 1
Samefld = NumLoci + 2
Maybefld = NumLoci + 3
```

```
Diff = Identity - MisMatch

If Identity = 0 Then
        ErrorCode = "Identity field not entered." + Chr(10)
End If
If MisMatch > Identity Then
        ErrorCode = ErrorCode + "Mis-Match must be less than Identity field." + Chr(10)
End If
If NumLoci = 0 Then
        ErrorCode = ErrorCode + "You must enter the number of Loci in data file." +
Chr(10)
End If
If NumSamp = 0 Then
        ErrorCode = ErrorCode + "You must enter the number of samples in data file!" +
Chr(10)
End If
If FileName = "" Then
        ErrorCode = ErrorCode + "You didn't choose a file!!" + Chr(10)
End If
If SaveFile = "" Then
        ErrorCode = ErrorCode + "You didn't name an output file." + Chr(10)
End If
If ErrorCode <> "" Then
        MsgBox ErrorCode, 16,
Else

Open FileName For Input As #1
LineNum = 0
For LineNum = 0 To NumSamp
        Input #1, LineStr
        Temp = Split(LineStr, Chr(9))
        For I = 0 To NumLoci
                B(LineNum, I) = Temp(I) 'brings in the data into array B
        Next I
        B(LineNum, Identfld) = ""
        B(LineNum, Samefld) = ""
        B(LineNum, Maybefld) = ""
Next LineNum
        B(0, Identfld) = "Identity"
        B(0, Samefld) = "Same"
        B(0, Maybefld) = "Maybes"
Close #1

Ct = 2
Loc = 1
```

```
B(1, Identfld) = 1
For LineNumA = 1 To NumSamp
        For LineNumB = 1 To NumSamp
        No = 0
     Yes = 0
     DiffLoc = ""
     If LineNumA <> LineNumB Then
        For Loc = 1 To NumLoci
        If B(LineNumB, Loc) <> B(LineNumA, Loc) And B(LineNumA, Loc) <> "--"
        And B(LineNumB, Loc) <> "--" Then
                No = No + 1
                DiffLoc = DiffLoc + B(0, Loc)
        End If
        If B(LineNumB, Loc) = B(LineNumA, Loc) And B(LineNumA, Loc) <> "--"
        Then
                Yes = Yes + 1
                End If
        Next Loc
        If No <= MisMatch And No > 0 And Yes >= Diff Then
                B(LineNumA, Maybefld) = B(LineNumA, Maybefld) + "_" +
                B(LineNumB, 0) + "(" + DiffLoc + ")"
        End If
        If No = 0 And Yes >= Identity Then
                B(LineNumA, Samefld) = B(LineNumA, Samefld) + "_" + B(LineNumB,
                0)
        If B(LineNumB, Identfld) <> "" Then
                B(LineNumA, Identfld) = B(LineNumB, Identfld)
        End If
        End If
        End If
        Next LineNumB
        If B(LineNumA, Identfld) = "" Then
                B(LineNumA, Identfld) = Str(Ct)
                Ct = Ct + 1
         End If
Next LineNumA

Open SaveFile For Output As #2
For lp = 0 To NumSamp
        LineStr = B(lp, 0) + ","
For lp2 = NumLoci + 1 To NumLoci + 3
        LineStr = LineStr + B(lp, lp2) + ","
Next lp2
Print #2, LineStr
Next lp
```

```
Close #2
End If
End Sub

Private Sub CmdOpen_Click()
With CommonDialog1
        .Filter = "text files (*.txt)|*TXT"
        .CancelError = False
        .DefaultExt = "txt"
        .InitDir = "c:\"
        .DialogTitle = "Open"
        .ShowOpen
End With 'closes statement
        FileName = CommonDialog1.FileName
        filetmp = Split(FileName, ".txt")
End Sub

Private Sub CmdSave_Click()
With CommonDialog1
        .Filter = "comma delimited (*.csv)|*CSV"
        .CancelError = False
        .DefaultExt = "csv"
        .InitDir = "c:\"
        .DialogTitle = "Save as"
        .FileName = filetmp(0) + "res"
        .ShowSave
End With
SaveFile = CommonDialog1.FileName
End Sub

Private Sub NumLociBox_Change()
If Val(NumLociBox.Text) = 0 And NumLociBox.Text <> "" And NumLociBox.Text <>
"0" Then
   MsgBox "Value must be a number", 16,
   NumLociBox.Text = "0"
End If

End Sub
```

APPENDIX II

SUPPLEMENTAL TABLE FROM CHAPTER 1

Table AII – 1. Probabilistic expectations of bears recovered in a Brownie recovery model (Brownie *et al.* 1987) for bears marked with tetracycline on Kuiu Island in 2000. f is the estimated recovery rate; S is the estimated survival rate.

Year marked	Number marked	Year of recovery		
		2000	2001	2002
2000	N_1	N_1f_1	$N_1f_1S_1$	$N_1f_1S_1S_2$
2001	0	0	0	0
2002	N_2			N_3f_3

APPENDIX III

SUPPLEMENTAL DESCRIPTIONS OF GENETIC METHODS

G-STATISTIC

I tested for significance of the differentiation with the log likelihood G-statistic (Goudet *et al.* 1996):

$$G = -2\sum_{l-1}^{nl}\sum_{k-1}^{np}\sum_{i-1}^{ni} n_{ikl} \ln\left(\frac{n_{ikl}}{n_k \bar{p}_i}\right)$$

where l was the number of loci, k was the number of populations, and p_i was the frequency of the ith allele. Multilocus genotypes were randomized between the two populations in a pairwise comparison, and a G-statistic was calculated for this randomization. The proportion of G-statistics from randomized data sets that were larger than that for the observed data set provided the probability that the null hypothesis was true, *i.e.*, the two populations were not differentiated (Goudet *et al.* 1996). Due to multiple comparisons, the α value was corrected using the standard Bonferroni procedure, and used as the significance criterion.

POPULATION BOTTLENECKS

The M-ratio is the average across all microsatellite loci of the ratio of the number of alleles (k) to the range of allele (r, in base pairs). The authors hypothesized that k decreased faster than r when the population was severely and quickly reduced in census size, as rare alleles, which did not generally define the extent of the range of alleles, were eliminated first. Garza and Williamson (2001) suggested that an M-ratio of 0.68 would signify that a significant bottleneck had occurred in a population. M-ratios may be >0.68 yet still significant, depending on the amount of time since the bottleneck occurred or if there is immigration from other populations. For example using this hypothesis, bottlenecks were identified populations considered endangered (*e.g.*, the Koala and northern elephant seal), and were not found in known thriving populations (*e.g.,* coyotes, harbor seal, Garza and Williamson (2001).

In Garza and Williamson's (2001) program, randomizations were used to create equilibrium distributions for the M-ratio from the microsatellite allelic data sets from each black bear island, and the observed M-ratio was compared with the distribution to determine the probability of the observed value. Garza and Williamson's (2001) program assumed a two-phase mutation model, and that 88% of mutations involved the addition or deletion of one repeat unit. The mean size of larger mutations was set to 1.2 microsatellite-repeat units. These parameters were found to best describe empirical data on mutational patterns of microsatellite loci (Garza and Williamson 2001).

STRUCTURE

In a given system, individuals could be grouped into K clusters. Each allele from an individual's genotype was treated as a random sample from a cluster's allele frequency distribution. Random draws of alleles from a frequency distribution, P, of an unknown population of origin, Z, described the probability distribution $Pr(X|Z,P,Q)$, where X represented the data (genotypes) and Q was the individual's proportional membership (assignment) in Z. The prior distributions, $Pr(Z)$ and $Pr(P)$, reflected the Hardy-Weinberg and linkage equilibrium models. The posterior distribution was: *Pr(Z,*

$P|X) \propto Pr(Z)\ Pr(P)\ Pr(X|Z,P)$. To ultimately infer K from the posterior distribution, $Pr(K|X) \propto Pr(X|K)Pr(K)$, a harmonic mean estimator was used estimate the prior, $Pr(X|K)$ (Pritchard *et al.* 2000). The posterior distribution used to infer Q is $Pr(Z,P,Q|X)$, which uses the priors $Pr(P,Q|X,Z)$ and $Pr\ (Z|X,P,Q)$. Arithmetic solutions of posterior distributions were not possible, and sampling from the priors was approximated using Markov chain Monte Carlo (MCMC), using Gibb's sampling to construct the chain (Pritchard *et al.* 2000). MCMC was used as a sampling tool that enables us to explore the posterior distributions (Sorensen and Gianola 2002). Markov chains of the parameters $((Z^{(1)}, P^{(1)}\ Q^{(1)}), (Z^{(2)},P^{(2)},Q^{(2)})\ldots(Z^{(m)},P^{(m)}\ Q^{(m)}))$ are generated until the posterior distributions were stable, which was dependent on the number of chains, m (Pritchard *et al.* 2000). In STRUCTURE, m was the burn-in period, which was the number of iterations required to stabilize the posterior distributions. The value of m was determined by evaluating whether the inferred values of the parameters (*e.g.*, $ln\ Pr(X|K)$) from the posterior distributions had converged. I chose 10^6 iterations for m, and used 10^6 iterations of the chain to approximate the posterior distributions. STRUCTURE determined the natural log of the probability of the data given a certain number of clusters ($ln\ Pr(X|K)$) for each value of K. I chose the value of K, that maximized this log likelihood. The probability of the data, given K (posterior probability of K) was determined by:

$$\Pr(X \mid K) = \frac{e^{\ln \Pr(X|K_{best})}}{\sum_{1}^{K} e^{\ln \Pr(X|K)}}$$

where K_{best} was the most likely value for K, and K was the maximum number of clusters which were evaluated in the scheme (Pritchard and Wen 2003).

APPENDIX IV

SUPPLEMENTAL GRAPHS FOR CHAPTER 2

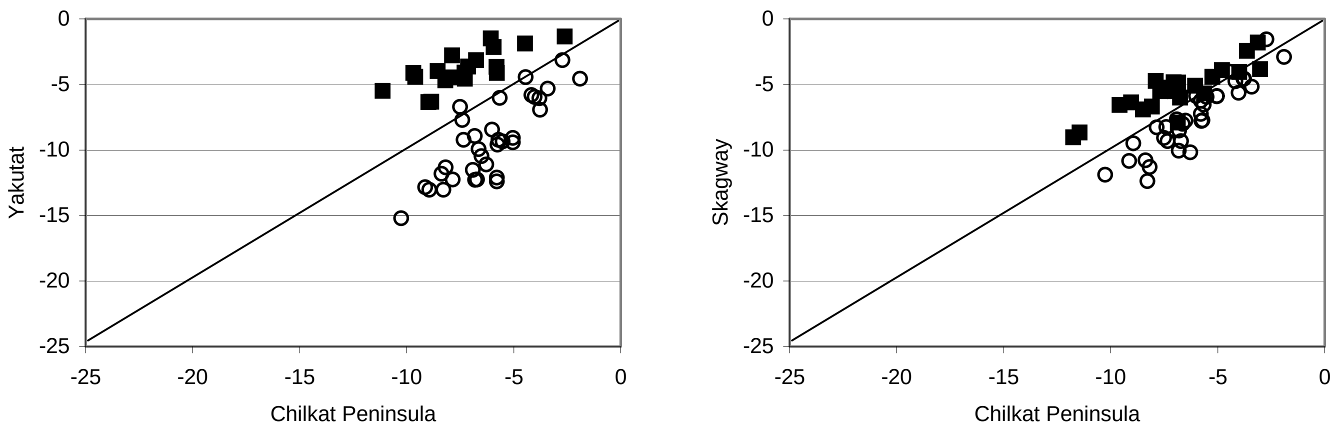
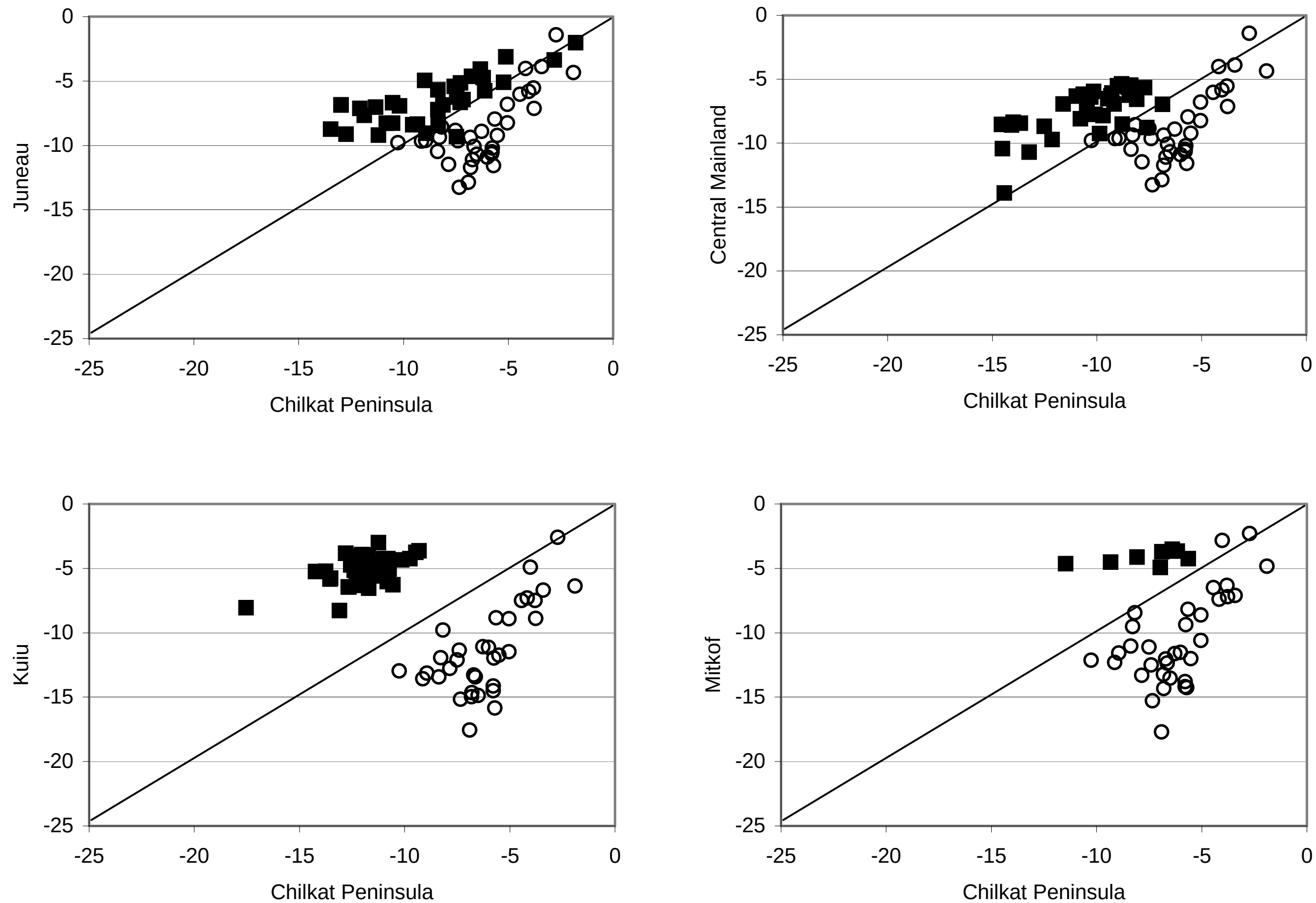
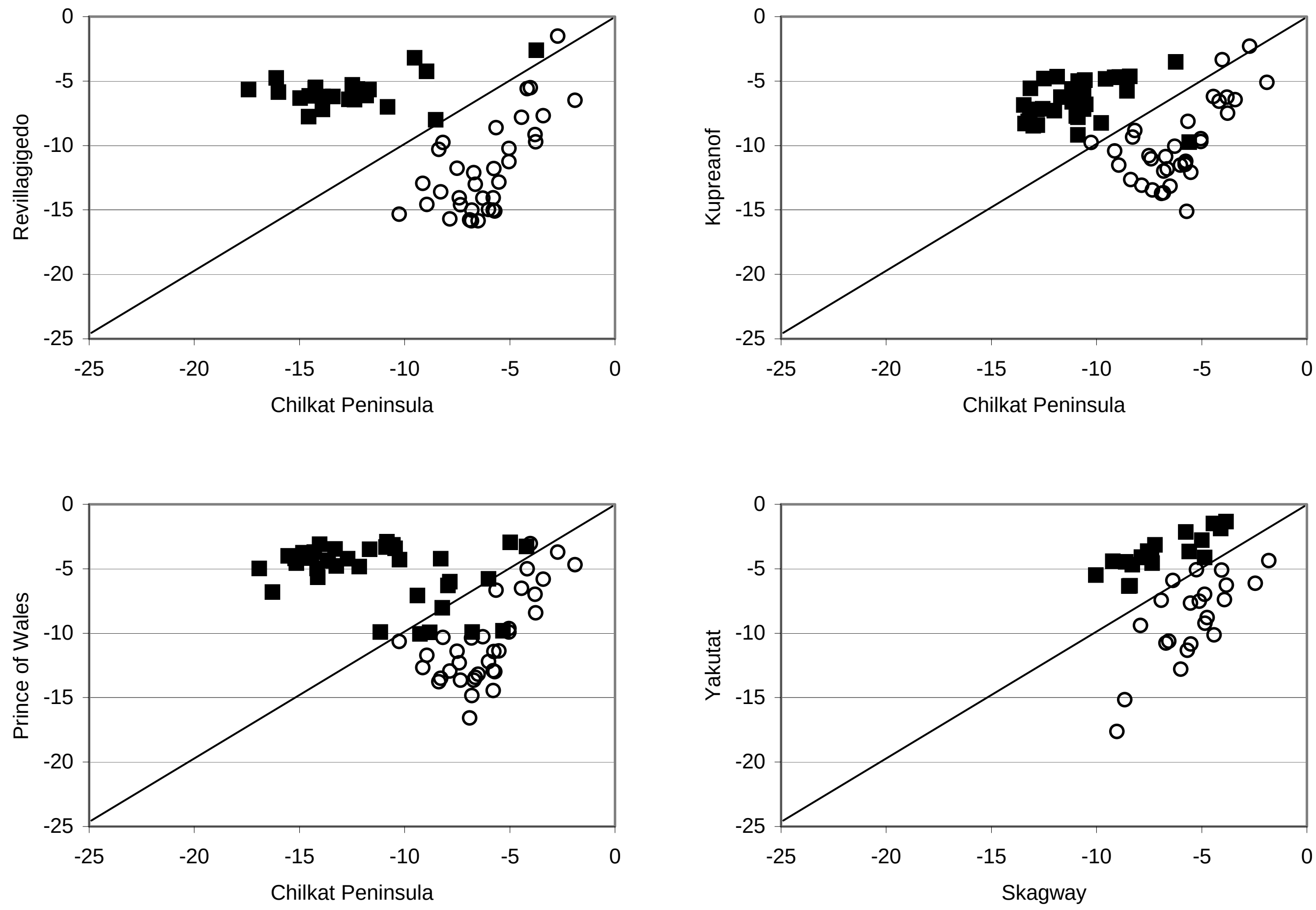


Figure A4 – 1. Assignment plots for all pair-wise comparisons (n = 55) of sampling regions in Southeast Alaska. X-axis the negative log likelihood of an individual being from the sampling region on the X axis relative to the negative log likelihood of an individual being from the sampling region on the Y-axis. Y-axis, vice versa



Juneau
Chilkat Peninsula
Central Mainland
Chilkat Peninsula
Kuiu
Chilkat Peninsula
Mitkof
Chilkat Peninsula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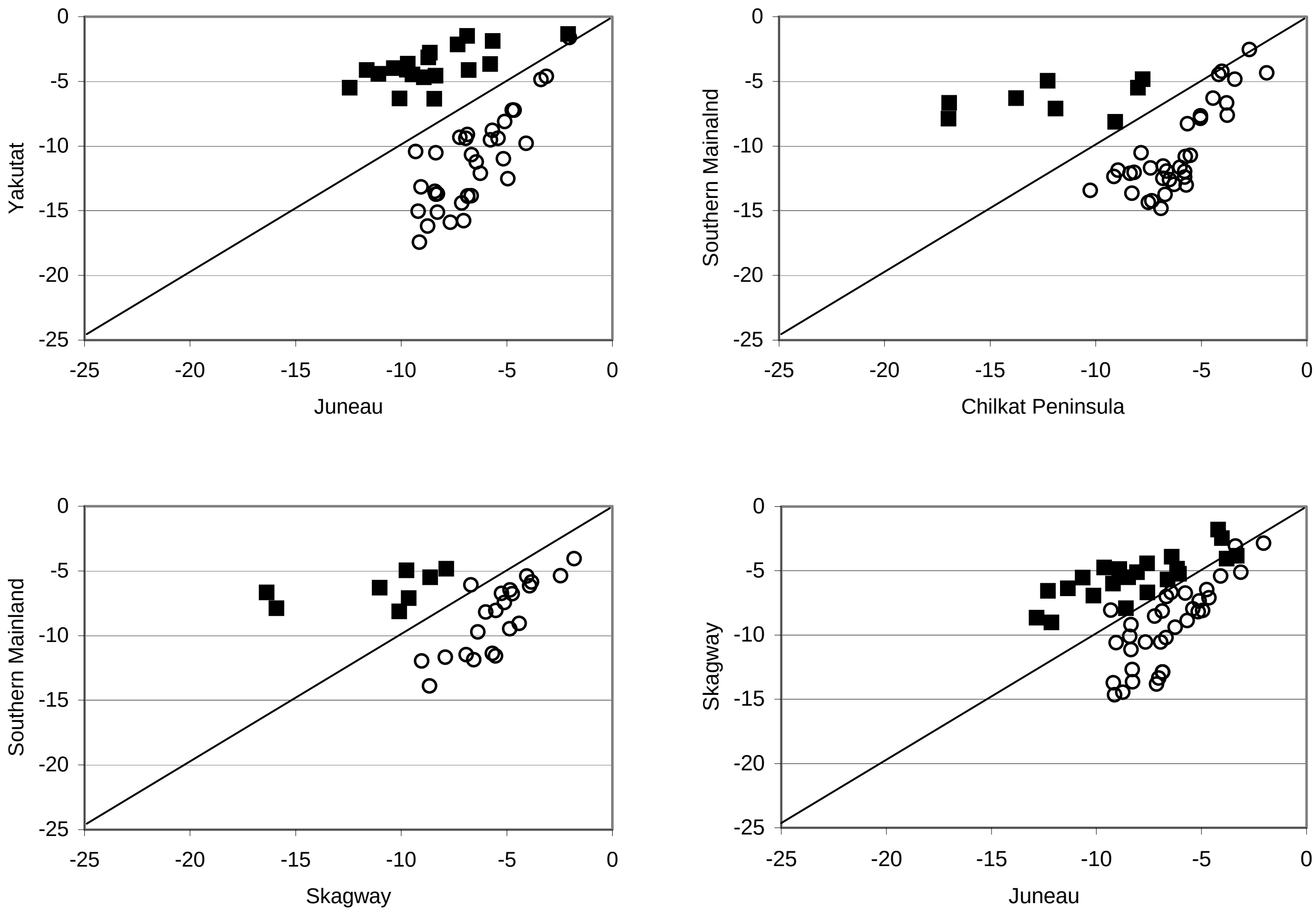
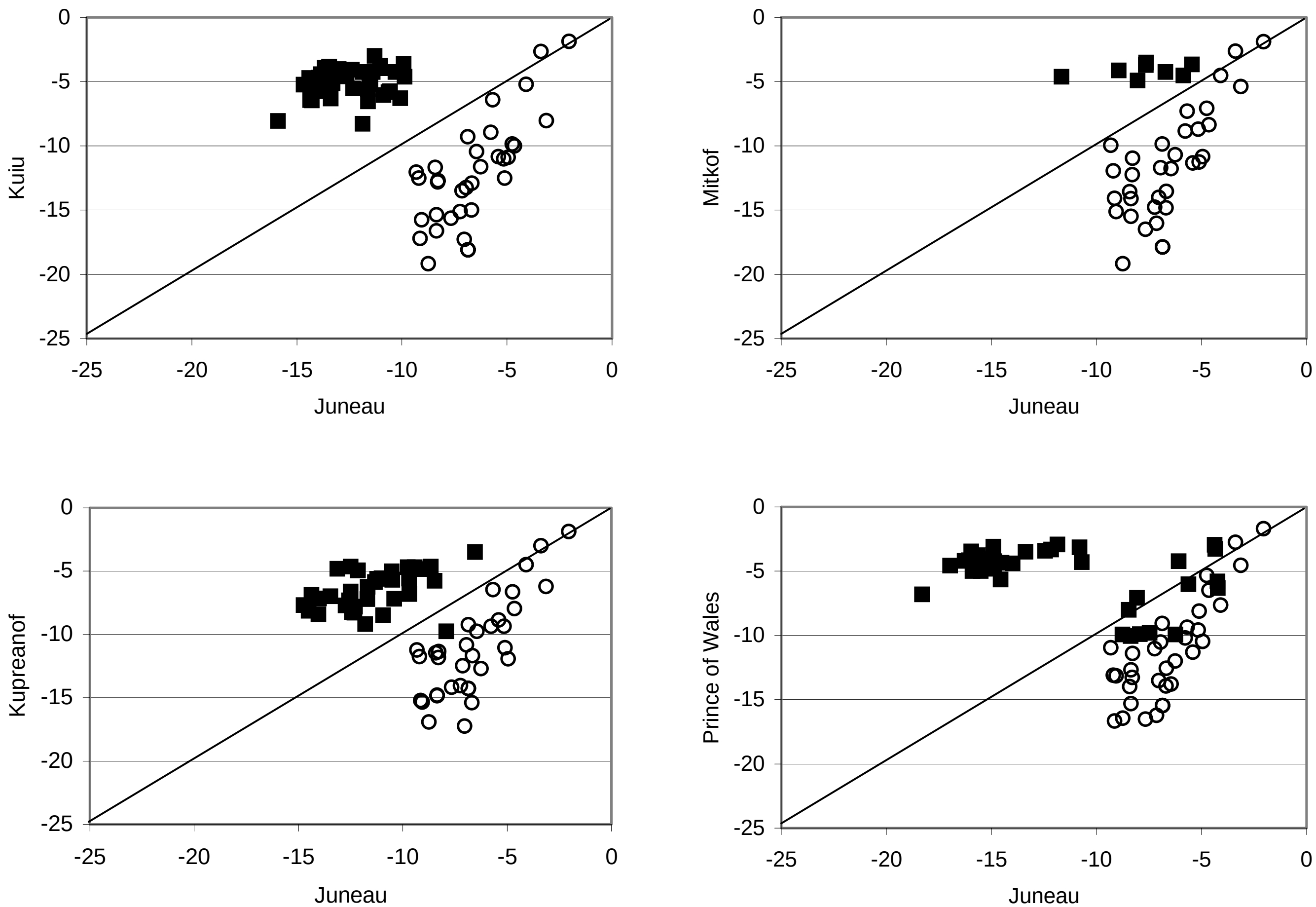
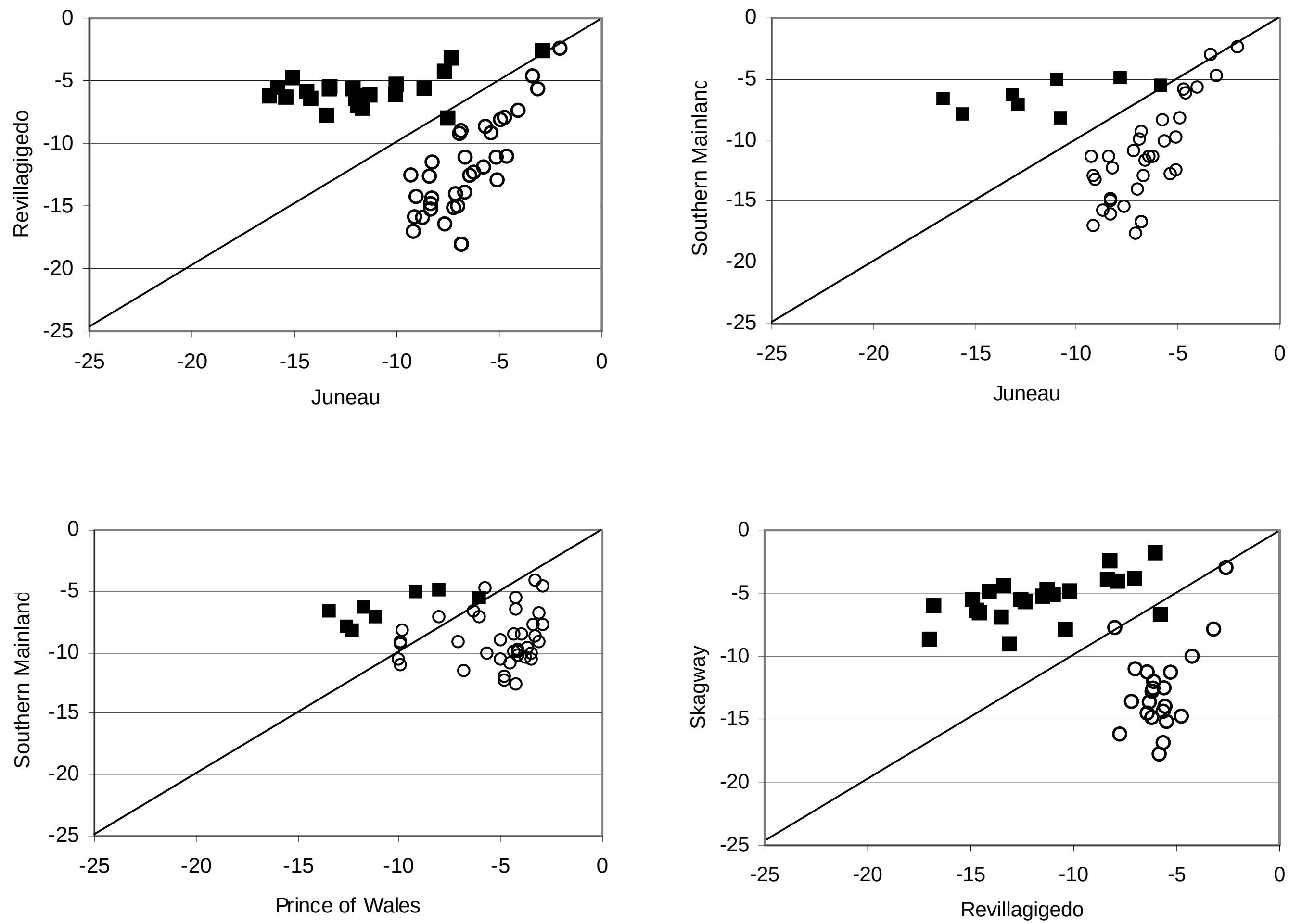
Chilkat Peninsula
Kupreanof
Chilkat Peninsula
Prince of Wales
Chilkat Peninsula
Yakutat
Skagway

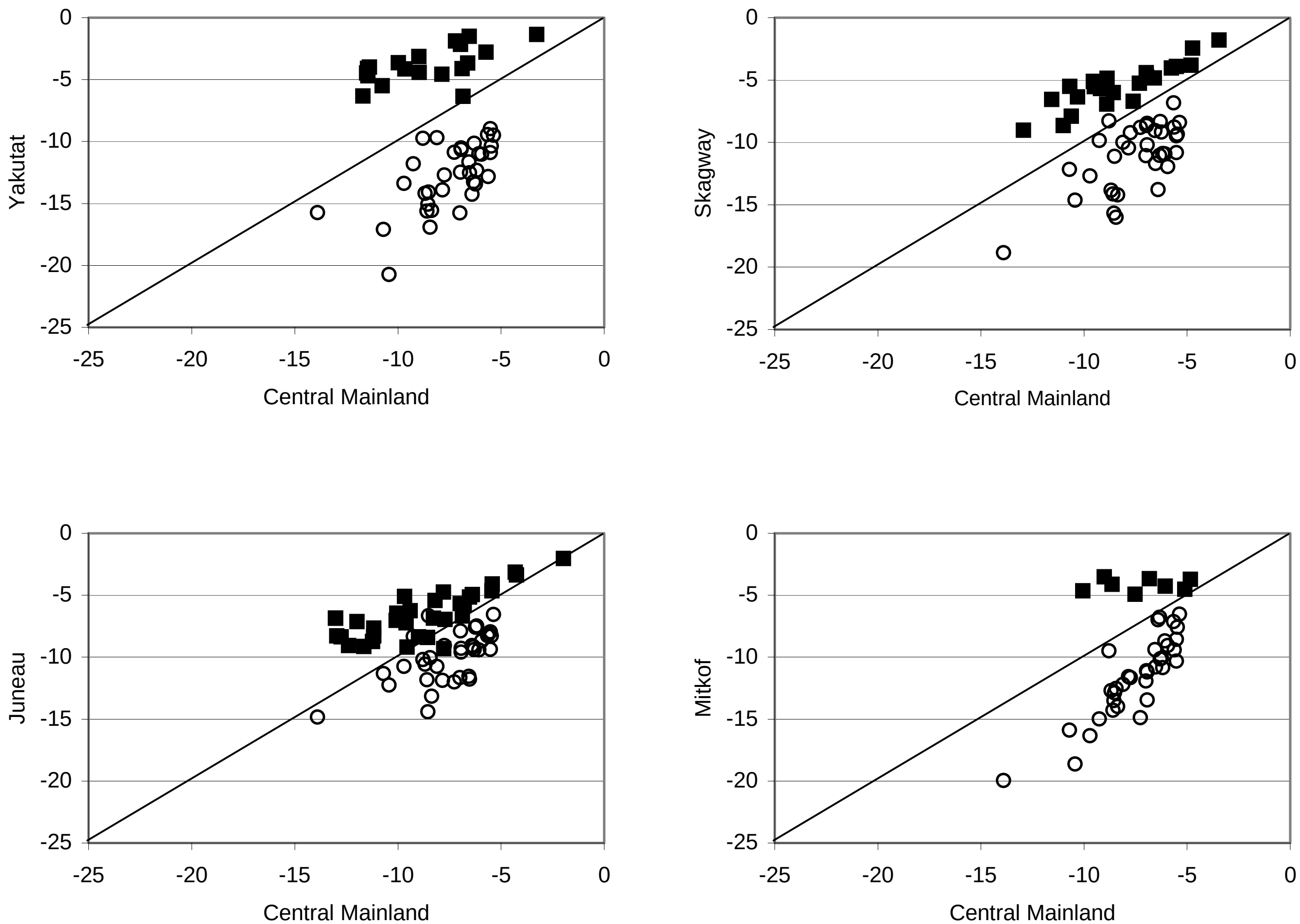


Yakutat
Juneau
Southern Mainalnd
Chilkat Peninsula
Southern Mainland
Skagway
Skagway
Juneau
0
-5
-10
-15
-20
-25


Kuiu
Juneau
Mitkof
Juneau
Kupreanof
Juneau
Prince of Wales
Juneau
0
-5
-10
-15
-20
-25



Revillagigedo
Juneau
Southern Mainlanc
Juneau
Southern Mainlanc
Prince of Wales
Skagway
Revillagigedo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Central Mainland
Skagway
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Juneau
Central Mainland
Mitkof
Central Mainland
0
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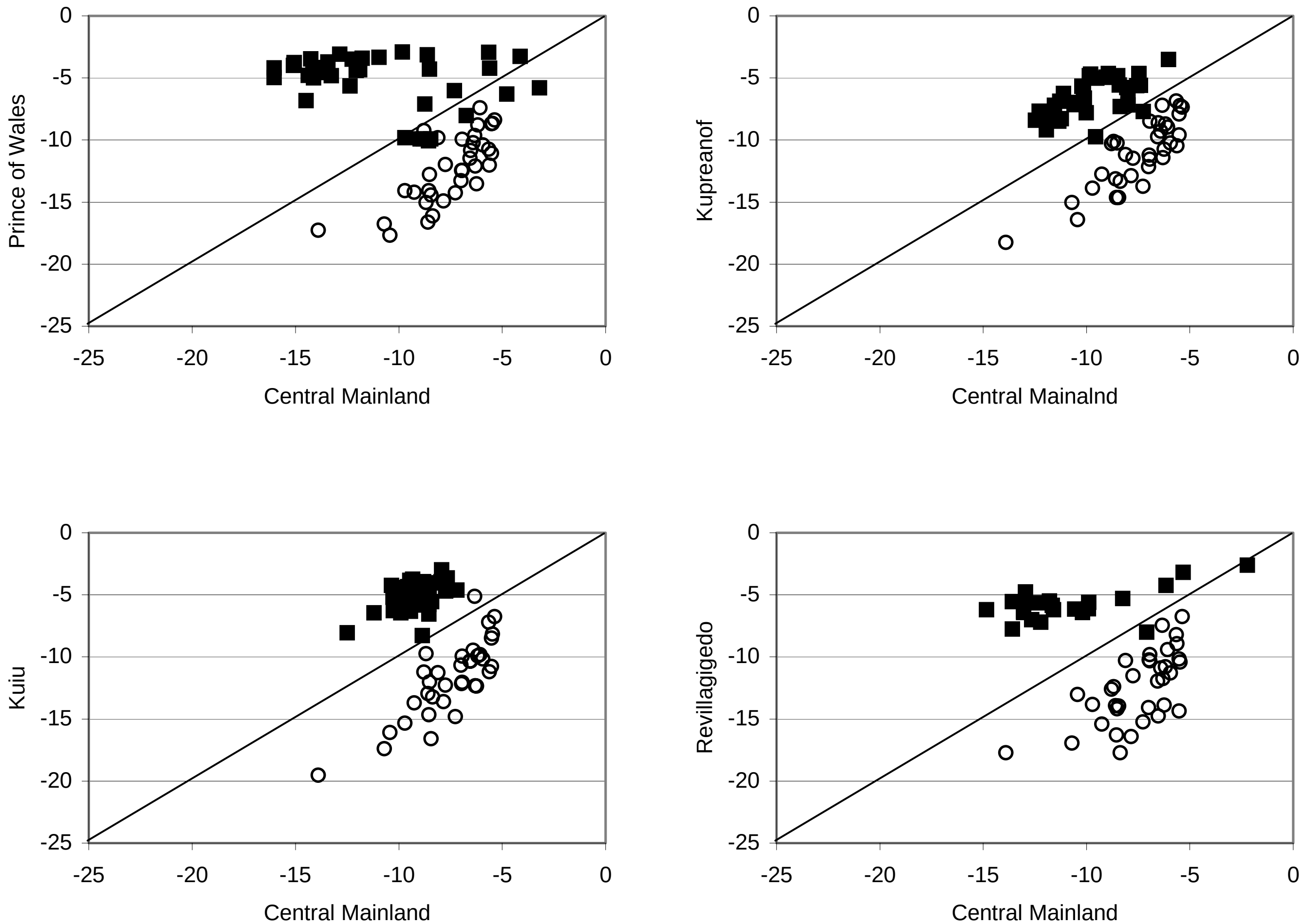
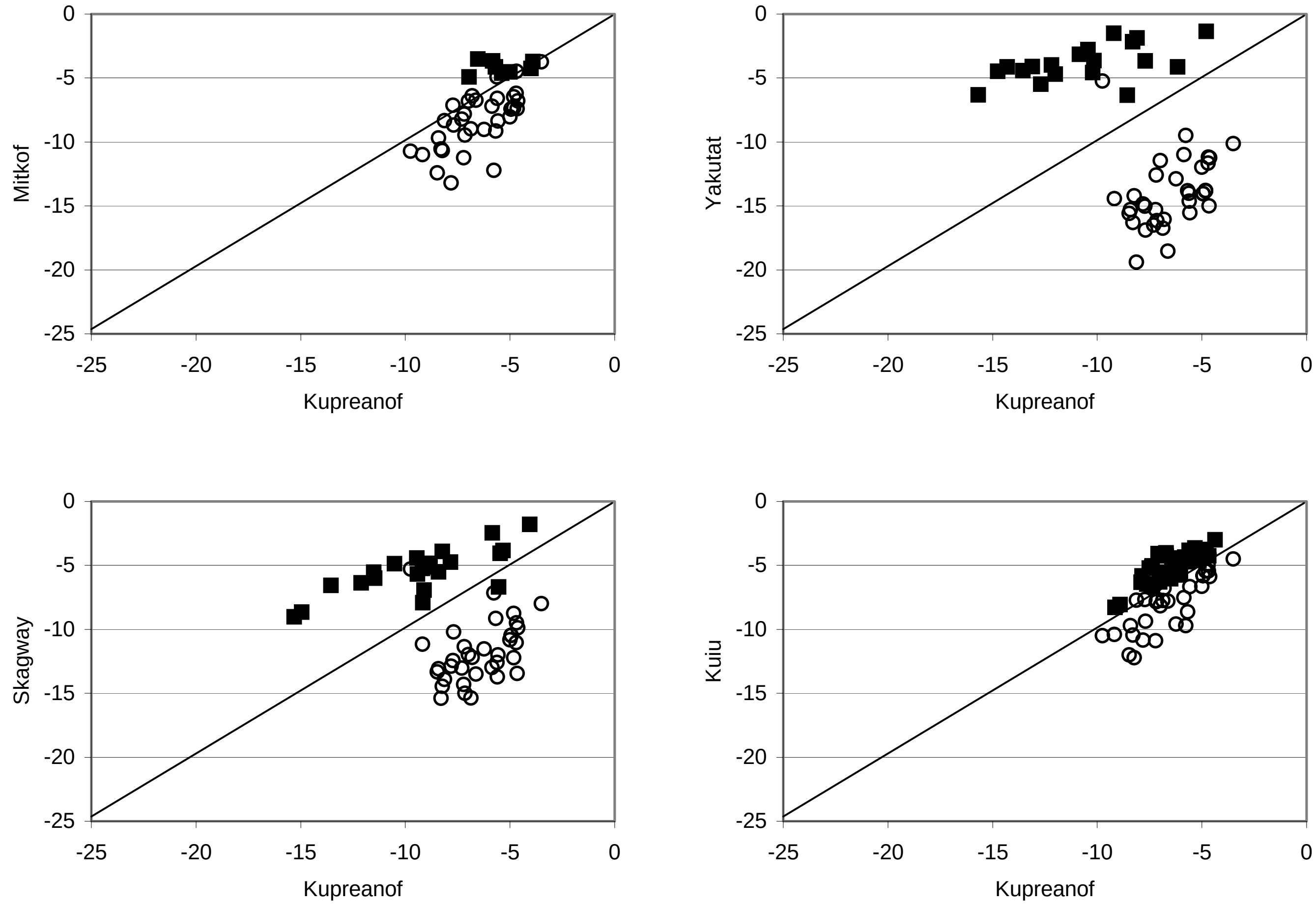
-15
-20
-25


Prince of Wales
Central Mainland
Kupreanof
Central Mainalnd
Kuiu
Central Mainland
Revillagigedo
Central Mainland



Mitkof
Kupreanof
Yakutat
Kupreanof
Skagway
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Kuiu
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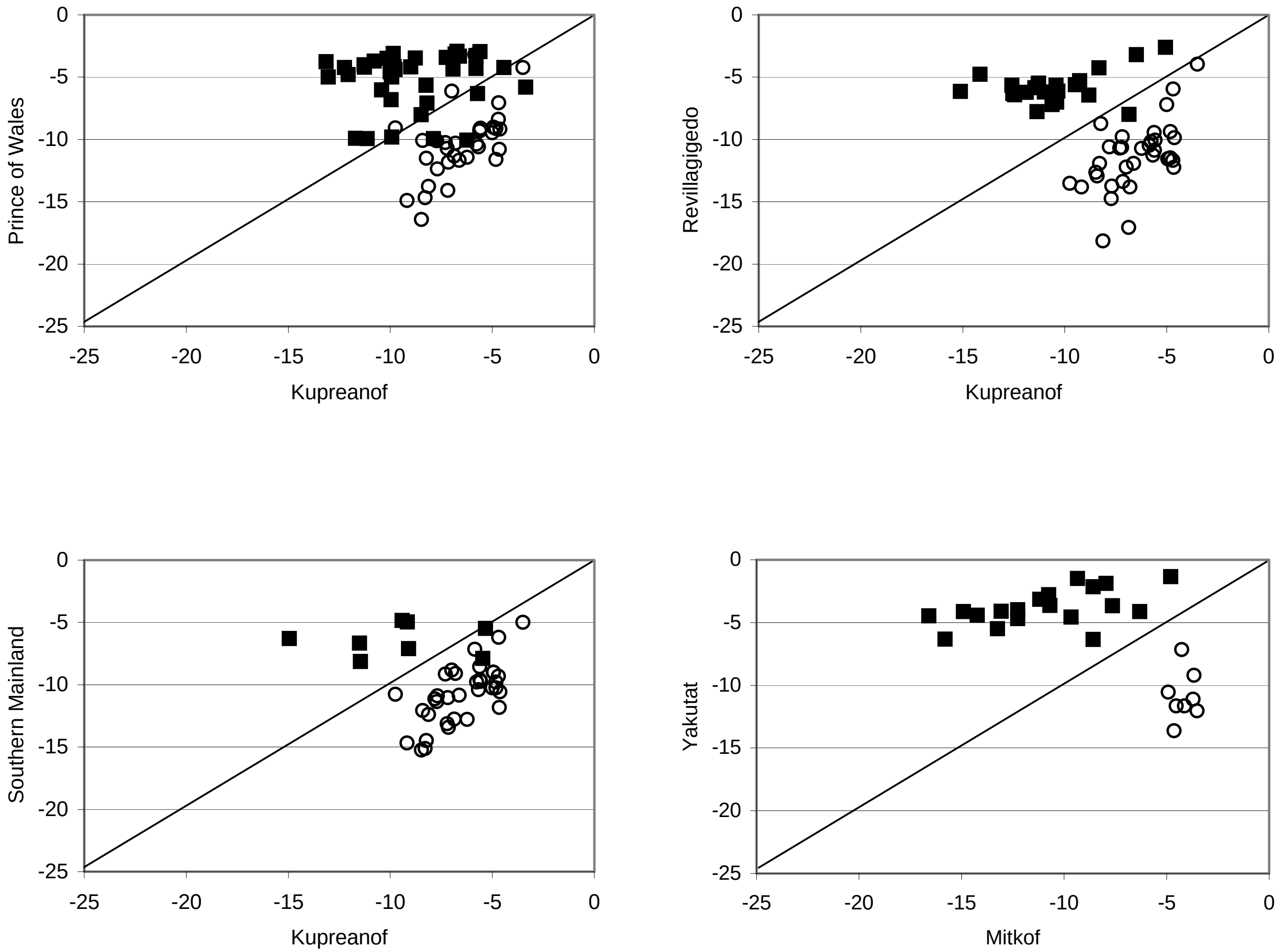
Prince of Wales
Kupreanof
Revillagigedo
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Southern Mainland
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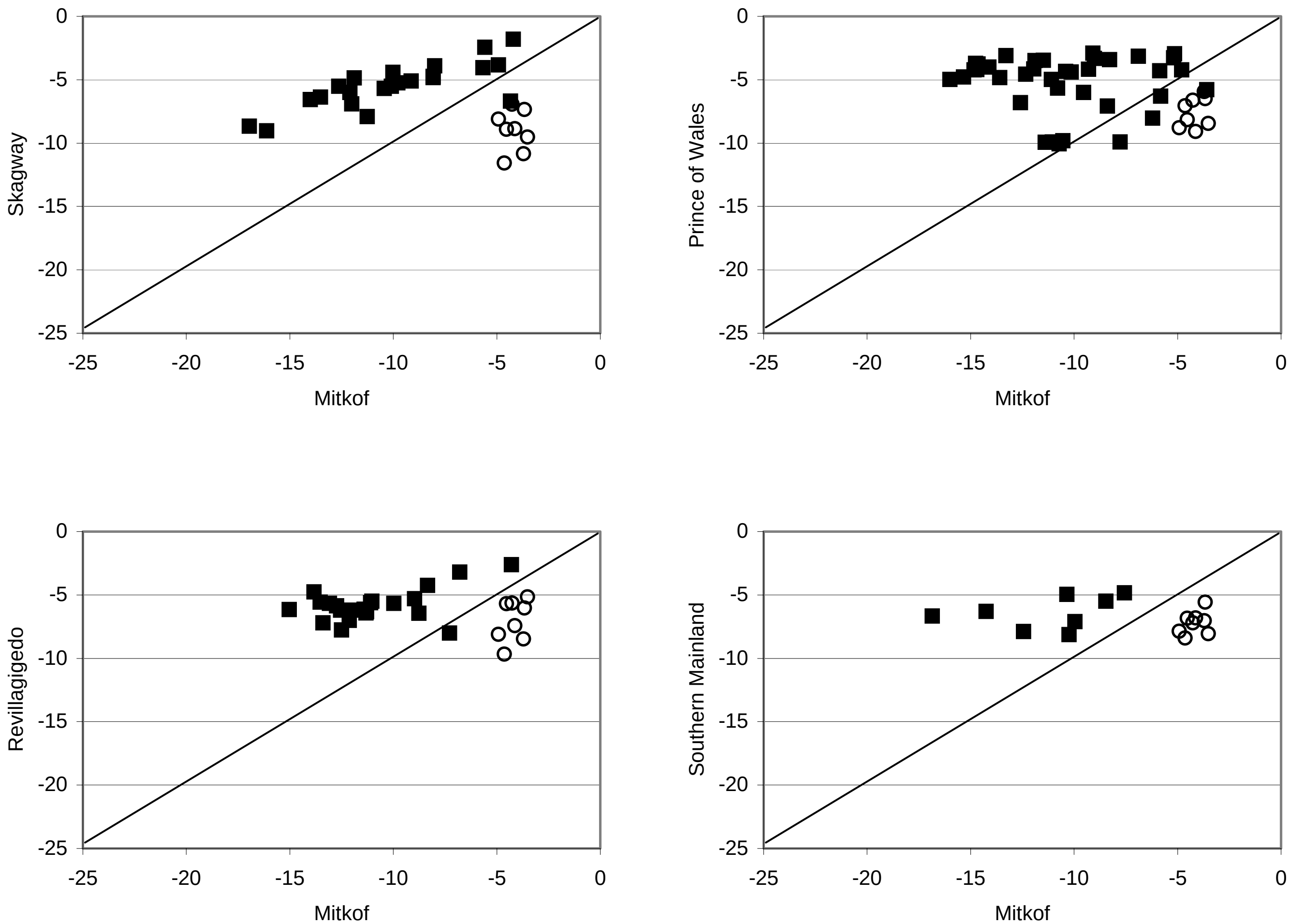
Yakutat
Mitkof



Skagway
Prince of Wales
Revillagigedo
Southern Mainland
Mitkof
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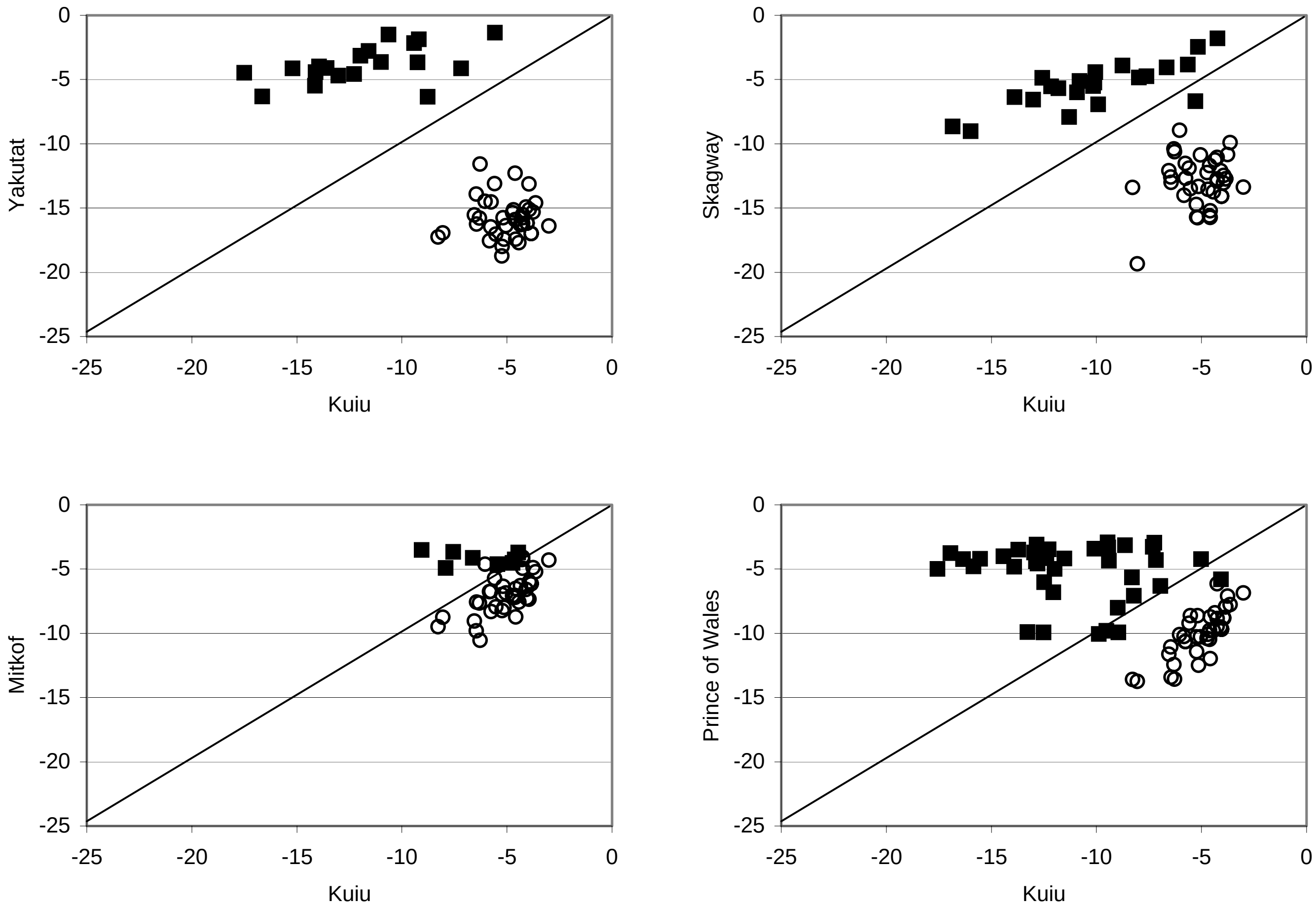
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Skagway
Mitkof
Prince of Wales
Kuiu
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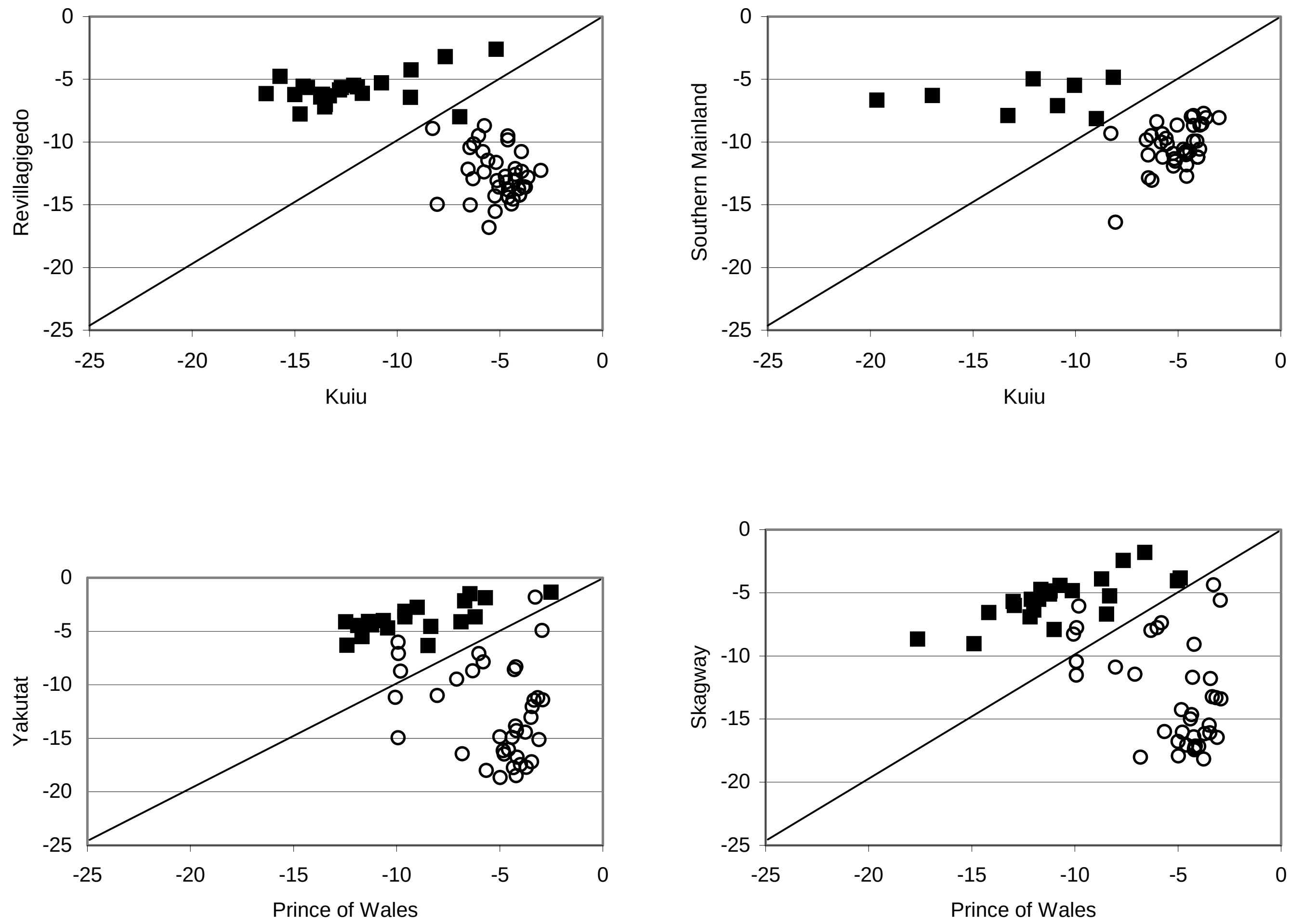
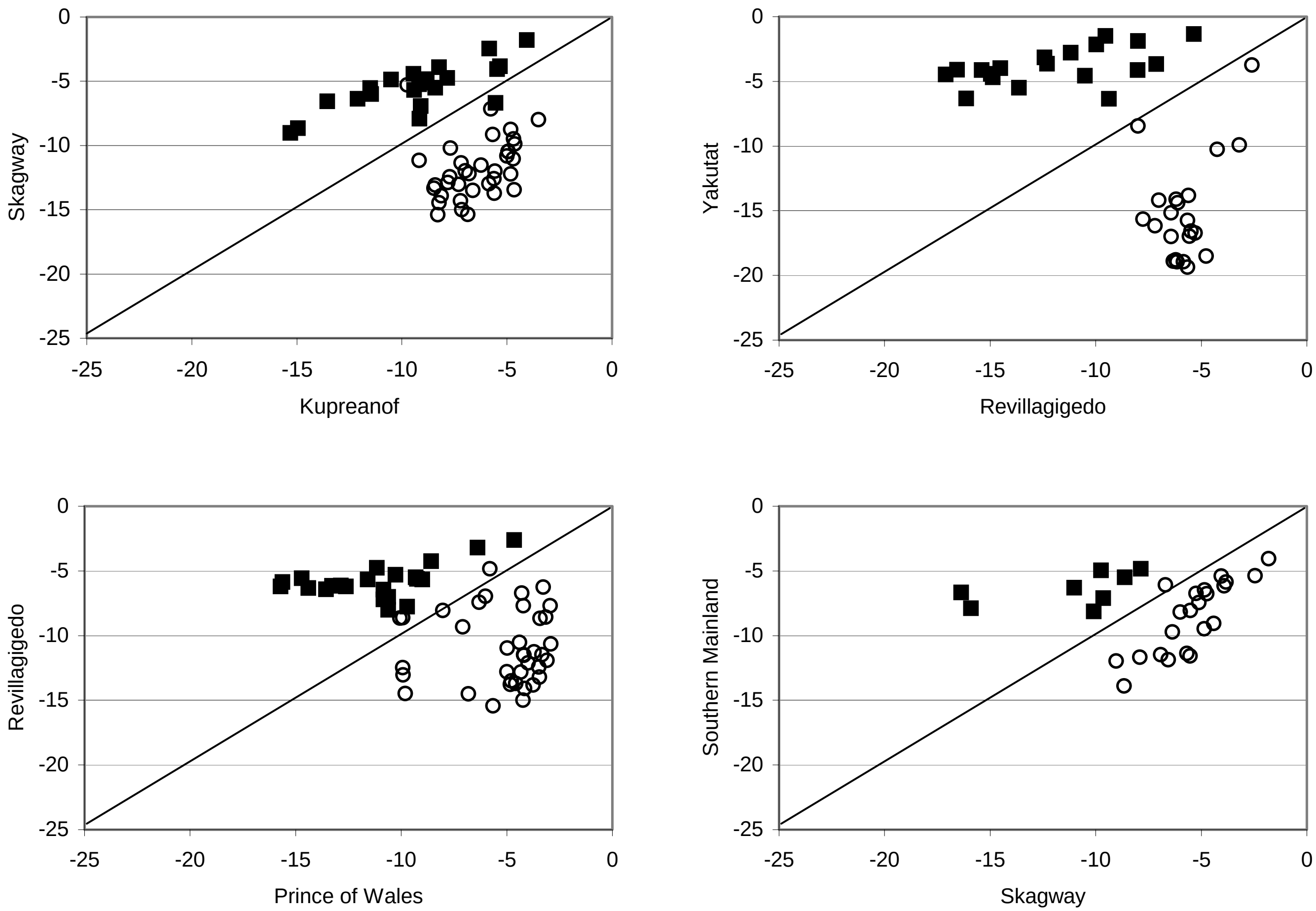

Revillagigedo
Kuiu
Southern Mainland
Kuiu
Yakutat
Prince of Wales
Skagway
Prince of Wales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Skagway
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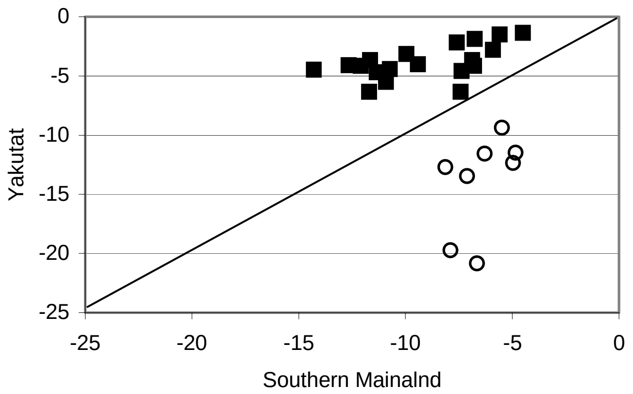
Kupreanof
Yakutat
Revillagigedo
Revillagigedo
Prince of Wales
Southern Mainland
Skagway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Yakutat
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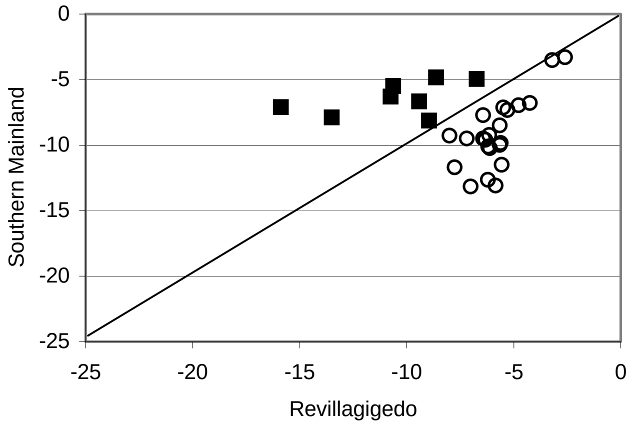
0
Southern Mainalnd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Southern Mainland
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-5
0
Revillagigedo

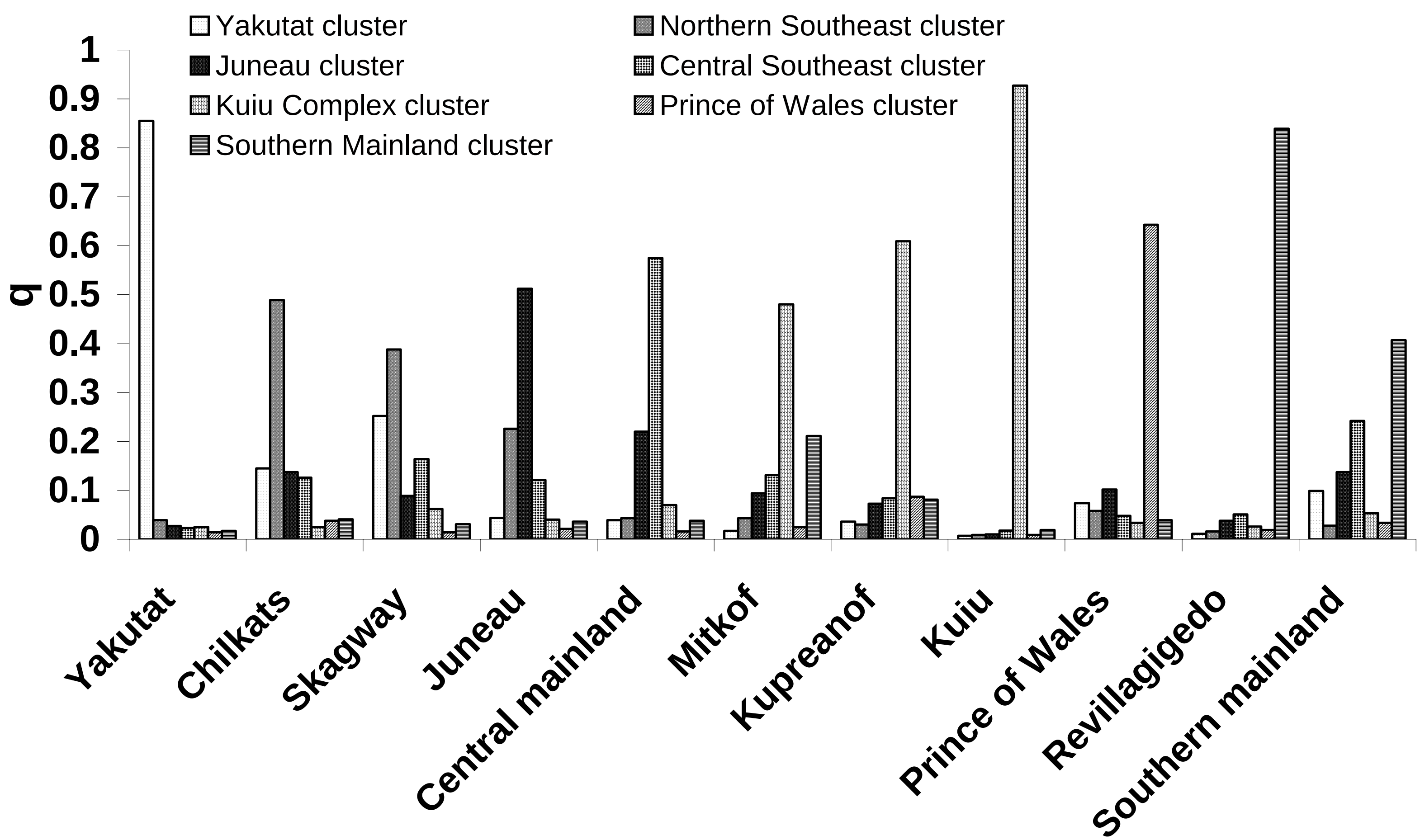


Figure A4 – 2.Average proportional membership (q) of individuals from sampling regions to the seven clusters identified by STRUCTURE.

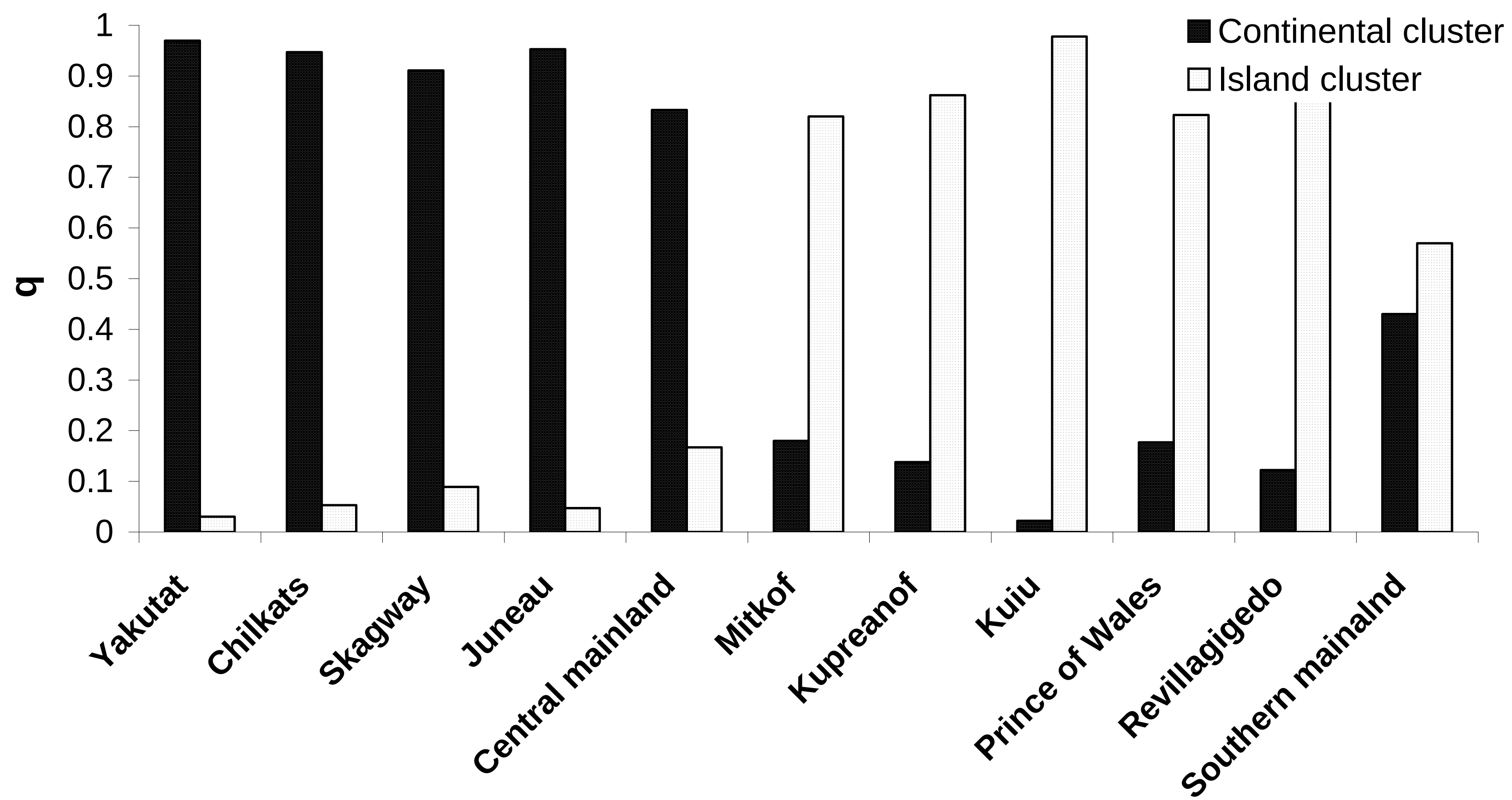


Figure A4 – 3. Average proportional membership (q) of individuals from sampling regions to two clusters identified by STRUCTURE.

APPENDIX V

Capture histories for each stream-year. 1 indicates capture, and 0 indicates not captured. The number following the series of 1's and 0's is the number of individuals with the particular capture history.

Saginaw Creek 2000

00000001	8	;
00000010	7	;
00000100	9	;
00000110	1	;
00000111	1	;
00001000	8	;
00001011	1	;
00001100	2	;
00001110	1	;
00010000	14	;
00011000	1	;
00011011	1	;
00011100	3	;
00100000	13	;
00100100	1	;
00100101	1	;
00101000	1	;
00110100	1	;
01000000	11	;
01001000	1	;
01011000	1	;
01101010	1	;
10000000	13	;
10000010	1	;
10010000	1	;
11000000	1	;
11010000	1	;
11100000	1	;
11111000	1	;

Saginaw Creek, July 1st – July 26th 2000

0001	17	;
0010	19	;
0011	3	;
0100	1	;
1011	1	;

Saginaw Creek, July 12th – Aug 1st 2000

0001	15	;
0010	16	;
0011	1	;
0100	18	;
0101	1	;
0110	2	;
0111	2	;
1000	1	;

Saginaw Creek, July 20th – Aug 6th 2000

0001	19	;
0010	16	;
0011	1	;
0100	12	;
0101	1	;
0110	1	;
1000	14	;
1001	1	;
1100	1	;
1101	1	;
1110	1	;
1111	1	;

Saginaw Creek, July 26th – Aug 13th 2000

1000	12	;
1000	15	;
1100	5	;
1000	15	;
1010	1	;
1100	1	;
1000	12	;
1001	1	;
1010	1	;
1011	1	;
1100	1	;
1101	1	;
1111	1	;

Saginaw Creek, August 1st – August 20th 2000

0001	11	;
0010	10	;
0011	3	;
0100	16	;
0110	3	;
0111	3	;
1000	14	;
1001	2	;
1010	2	;
1101	1	;
1110	1	;

Saginaw Creek, August 7th – August 26th 2000

0001	8	;
0010	11	;
0011	2	;
0100	10	;
0101	2	;
0110	2	;
0111	1	;
1000	16	;
1010	1	;
1100	3	;
1101	1	;
1110	3	;

Saginaw Creek, August 13th – September 1st 2000

0001	7	;
0010	8	;
0100	11	;
0101	1	;
0110	1	;
0111	1	;
1000	13	;
1010	1	;
1011	2	;
1100	5	;
1110	1	;

Security Creek

0000000010	8	;
0000000100	6	;

0000001000	4	;
0000010000	11	;
0000010100	1	;
0000100000	9	;
0000101000	1	;
0000110000	1	;
0001000000	7	;
0010000000	5	;
0011000000	1	;
0100000000	2	;
1000000000	3	;
1000100000	1	;
1010000000	1	;

Cabin Creek 2000

0001	5	;
0010	8	;
0011	2	;
0100	2	;
1000	3	;
1001	2	;
1011	1	;
1111	1	;

Portage Creek 2000

000001	8	;
000010	2	;
000100	5	;
000101	1	;
001000	4	;
010000	2	;
010010	1	;
100000	5	;

Upper Kadake Creek 2000

000001	8	;
000010	6	;
000100	3	;
000101	2	;
001000	3	;
001001	2	;
010000	1	;

100000	9	;
101000	2	;

Lower Kadake Creek 2000

000001	8	;
000010	6	;
000100	3	;
000101	2	;
001000	3	;
001001	2	;
010000	1	;
100000	9	;
101000	2	;

Saginaw Creek 2002

000000001	5	;
000000010	6	;
000000100	2	;
000001000	8	;
000001100	2	;
000010000	7	;
000010010	1	;
000010110	1	;
000011000	1	;
000100000	12	;
000110000	1	;
001000000	9	;
001000010	1	;
001001000	1	;
001100000	1	;
010000000	8	;
010000100	1	;
010100000	1	;
011000000	1	;
011100000	1	;
100000000	8	;
100000010	1	;
100000110	1	;
101000000	2	;

Skinny Rowan Creek 2002

000000010	2	;
000000100	3	;

000000110	1	;
000001000	2	;
000010000	1	;
000100000	3	;
001000000	2	;
001000100	1	;
001001000	1	;
001100000	1	;
001110111	1	;
001111100	1	;
011000100	1	;
011111110	1	;
100100110	1	;

Cabin Creek 2002

00000001	3	;
00000010	6	;
00000100	3	;
00001000	3	;
00010000	1	;
00100000	1	;
00101011	1	;
00110000	1	;
01000000	3	;
01011010	1	;
01100010	1	;
10000000	1	;
10000010	2	;
10010000	1	;
11110011	1	;

Portage Creek 2002

00000001	1	;
00000010	3	;
00000011	1	;
00000100	1	;
00000111	1	;
00001110	1	;
00010000	1	;
00100000	1	;
00100001	1	;
01000000	1	;
01100000	1	;

10000000	1	;

Rowan Creek 2002

00000001	1	;
00000010	4	;
00000010	1	;
00000011	1	;
00000100	4	;
00000101	1	;
00000110	1	;
00001000	7	;
00001010	1	;
00010000	10	;
00010010	1	;
00100000	11	;
00100100	1	;
00101100	1	;
00110001	1	;
00111010	1	;
01000000	11	;
01010011	1	;
01110000	2	;
10000000	6	;
10000001	1	;
10000010	1	;
10000100	1	;
10001000	1	;
10010000	1	;
10110000	1	;
11000000	2	;
11100000	1	;

APPENDIX VI

SUPPLEMENTAL TABLES AND FIGURES FOR CHAPTER 3.

Table A6 – 1. CJS models for black bears on Cabin Creek 2000. All tested models with ΔAICc ≤ 5.0 and *φ*(t)*p*(t) are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (T) indicates a trend in the parameter over time, where (2T) refers to two groupings into which intervals were collapsed. (t) refers to a time-specific (non-linear) effect on the parameter, where (3t) refers to three groupings of intervals. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
***φ*(.)*p*(.)**	42.103	0.00	0.49324	1.0000	1	12.017
φ(.)*p*(T)	43.608	1.50	0.23248	0.4713	2	11.090
φ(.)*p*(2T)	43.773	1.67	0.21405	0.4340	2	11.255
φ(.)*p*(3t)	46.309	4.21	0.06024	0.1221	3	11.089
***φ*(t)*p*(t)§**	49.281	7.18	0.01344	0.0276	4	11.050

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 2. CJS models for black bears on Cabin Creek 2002. Only models with ΔAICc ≤ 3.0 are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (t) refers to a time-specific (non-linear) effect on the parameter. (T) indicates a trend in the parameter over time, where (XT) refers to the number of groupings into which intervals were collapsed. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
***φ*(t)*p*(t)§**	94.805	0.00	0.47398	1.0000	7	47.994
***φ*(.)*p*(.)**	97.063	0.00	0.29127	1.0000	2	63.331
φ(.)*p*(4T)	97.895	0.83	0.19212	0.6596	3	61.831
φ(.)*p*(2T)	98.238	1.17	0.16190	0.5558	3	62.173
φ(.)*p*(6T)	98.558	1.5.0	0.13792	0.4735	3	62.493
φ(.)*p*(5T)	98.905	1.84	0.11597	0.3982	3	62.840
φ(.)*p*(3T)	99.185	2.12	0.10081	0.3461	3	63.120

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 3. CJS models for black bears on Portage Creek 2000. Only one model had an ΔAICc ≤ 3.0; *φ* (t)*p*(t) is also presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (t) refers to a time-specific (non-linear) effect on the parameter. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
***φ* (.)*p*(.)**	19.946	0.00	0.8751	1.0000	1	8.51
***φ* (t)*p*(t)§**	19.065	0.00	0.5766	1.0000	3	5.17

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 4. CJS models for black bears on Portage Creek 2002. Only models with ΔAICc ≤ 3.0 are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (T) indicates a trend in the parameter over time, where (XT) refers to the number of groupings into which intervals were collapsed. (t) refers to a time-specific (non-linear) effect on the parameter, where (2t) refers to two groupings of intervals. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
***φ*(.)*p*(.)**	39.652	0.00	0.11585	1.0000	2	21.979
φ(T)*p*(.)	40.088	0.44	0.09316	0.8042	3	19.425
φ(6T)*p*(.)	40.101	0.45	0.09257	0.7991	3	19.438
φ(.)*p*(2T)	40.106	0.45	0.09233	0.7970	3	19.443
φ(4T)*p*(.)	40.206	0.55	0.08782	0.7581	3	19.544
φ(3T)*p*(.)	40.232	0.58	0.08671	0.7485	3	19.569
φ(5T)*p*(.)	40.297	0.64	0.08394	0.7246	3	19.634
φ(.)*p*(4T)	41.071	1.42	0.05698	0.4919	3	20.409
φ(.)*p*(T)	41.101	1.45	0.05614	0.4846	3	20.438
φ(.)*p*(5T)	41.239	1.59	0.05240	0.4523	3	20.576
***φ*(t)*p*(t)§**	41.257	1.60	0.04937	0.4483	5	12.986
φ(.)*p*(3T)	41.855	2.20	0.03851	0.3324	3	21.192
φ(.)*p*(2t)	42.067	2.41	0.03464	0.2990	3	21.404

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 5. CJS models for black bears on Saginaw Creek 2000. Only models with ΔAICc ≤ 3.0 and *φ*(t)*p*(t) are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (T) indicates a trend in the parameter over time, where (XT) refers to the number of groupings into which intervals were collapsed. (t) refers to a time-specific (non-linear) effect on the parameter, where (Xt) refers to three groupings of intervals. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
***φ*(.)*p*(.)**	248.702	0.00	0.08107	1.0000	2	80.431
φ(3T)*p*(3T)	249.510	0.81	0.05413	0.6677	4	77.025
φ(4T)*p*(3T)	250.113	1.41	0.04004	0.4939	4	77.628
φ(.)*p*(5T)	250.146	1.44	0.03938	0.4858	3	79.784
φ(3T)*p*(5T)	250.231	1.53	0.03774	0.4655	4	77.746
φ(.)*p*(3T)	250.235	1.53	0.03767	0.4647	3	79.873
φ(4T)*p*(5T)	250.245	1.54	0.03747	0.4622	4	77.761
φ(2T)*p*(2T)	250.287	1.58	0.03670	0.4527	4	77.802
φ(.)*p*(3t)	250.300	1.60	0.03647	0.4499	4	77.815
φ(.)*p*(6T)	250.336	1.63	0.03581	0.4417	3	79.974
φ(T)*p*(3T)	250.354	1.65	0.03549	0.4378	4	77.870
φ(T)*p*(5T)	250.484	1.78	0.03326	0.4103	4	77.999
φ(5T)*p*(3T)	250.487	1.78	0.03321	0.4097	4	78.002
φ(.)*p*(2T)	250.609	1.91	0.03124	0.3854	3	80.247
φ(.)*p*(2t)	250.609	1.91	0.03124	0.3854	3	80.247
φ(.)*p*(4T)	250.610	1.91	0.03123	0.3852	3	80.248
φ(2T)*p*(.)	250.728	2.03	0.02944	0.3631	3	80.366
φ(.)*p*(4t)	250.751	2.05	0.02909	0.3588	3	80.389
φ(2T)*p*(5T)	251.096	2.39	0.02449	0.3021	4	78.612
φ(2T)*p*(3T)	251.218	2.52	0.02304	0.2842	4	78.733
φ(T)*p*(6T)	251.268	2.57	0.02247	0.2772	4	78.784
φ(4T)*p*(4T)	251.324	2.62	0.02185	0.2695	4	78.839
φ(.)*p*(3t)	251.435	2.73	0.02067	0.2550	4	78.951
φ(T)*p*(T)	251.494	2.79	0.02008	0.2477	4	79.009
φ(3T)*p*(4T)	251.498	2.80	0.02004	0.2472	4	79.013
φ(T)*p*(4T)	251.740	3.04	0.01775	0.2189	4	79.255
***φ*(t)*p*(t)**	267.101	18.4	0.00001	0.0001	13	73.960

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 6. CJS models for black bears on Saginaw Creek 2002. Only models with ΔAICc ≤ 3.0 are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t) *p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (t) refers to a time-specific (non-linear) effect on the parameter. (T) indicates a trend in the parameter over time, where (XT) refers to the number of groupings into which intervals were collapsed. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	Δ AICc	AICc weight	Model likelihood	#Parameters	Deviance
***φ*(t)*p*(t)§**	**153.525**	**0.00**	**0.45811**	**1.0000**	**8**	**29.972**
***φ*(.)*p*(.)**	**158.219**	**0.00**	**0.08088**	**1.0000**	**2**	**48.175**
φ(3T)*p*(.)	158.751	0.53	0.06200	0.7665	3	46.576
φ(5T)*p*(6T)	158.935	0.72	0.05653	0.6989	4	44.584
φ(7T)*p*(.)	159.034	0.81	0.05383	0.6655	3	46.859
φ(6T)*p*(.)	159.063	0.84	0.05305	0.6559	3	46.888
φ(5T)*p*(4T)	159.205	0.99	0.04941	0.6109	4	44.854
φ(.)*p*(5T)	159.409	1.19	0.04462	0.5517	3	47.234
φ(4T)*p*(.)	159.411	1.19	0.04456	0.5509	3	47.237
φ(.)*p*(3T)	159.632	1.41	0.03991	0.4934	3	47.458
φ(5T)*p*(2T)	159.714	1.49	0.03831	0.4736	4	45.363
φ(5T)*p*(T)	159.813	1.59	0.03645	0.4507	4	45.462
φ(5T)*p*(7T)	160.064	1.84	0.03215	0.3975	4	45.713
φ(.)*p*(T)	160.085	1.87	0.03182	0.3934	3	47.91
φ(.)*p*(6T)	160.093	1.87	0.03170	0.3919	3	47.918
φ(3T)*p*(6T)	160.112	1.89	0.03139	0.3881	4	45.761
φ(2T)*p*(.)	160.129	1.91	0.03113	0.3849	3	47.954
φ(3T)*p*(2T)	160.211	1.99	0.02988	0.3694	4	45.86
φ(.)*p*(4T)	160.229	2.01	0.02961	0.3661	3	48.054
φ(5T)*p*(5T)	160.293	2.07	0.02868	0.3546	4	45.942
φ(.)*p*(2T)	160.344	2.12	0.02796	0.3457	3	48.17
φ(5T)*p*(3T)	160.441	2.22	0.02663	0.3292	4	46.09
φ(3T)*p*(T)	160.483	2.26	0.02608	0.3224	4	46.131
φ(T)*p*(T)	160.764	2.54	0.02266	0.2802	4	46.413
φ(7T)*p*(T)	160.783	2.56	0.02245	0.2776	4	46.432
φ(6T)*p*(T)	160.877	2.66	0.02141	0.2647	4	46.526
φ(4T)*p*(2T)	161.012	2.79	0.02002	0.2475	4	46.66

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 7. CJS models for black bears on Lower Kadake Creek 2000. Only models with ΔAICc ≤ 3.0 are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (T) indicates a trend in the parameter over time, where (3T) refers to the three groupings into which intervals were collapsed. (t) refers to a time-specific (non-linear) effect on the parameter, where (2t) refers to two groupings of intervals. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
***φ*(t)*p*(t)§**	34.327	0.00	0.99633	1.0000	2	5.9916
***φ*(.)*p*(.)**	48.500	0.00	0.22704	1.0000	2	20.164
φ(T)*p*(.)	49.577	1.08	0.13247	0.5835	3	18.763
φ(.)*p*(T)	49.708	1.21	0.12409	0.5466	3	18.893
φ(3T)*p*(.)	49.720	1.22	0.12331	0.5431	3	18.906
φ(.)*p*(3T)	49.927	1.43	0.11122	0.4899	3	19.112
φ(.)*p*(2t)	50.536	2.04	0.08202	0.3613	3	19.722

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 8. CJS models for black bears on Security Creek 2000. Only models with ΔAICc ≤ 3.0 are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (T) indicates a trend in the parameter over time, where (XT) refers to the number of groupings into which intervals were collapsed. (t) refers to a time-specific effect on the parameter. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
φ(3T)*p*(.)	56.641	0.00	0.09409	1.0000	3	15.207
φ(4T)*p*(.)	57.089	0.45	0.07522	0.7994	3	15.655
φ(5T)*p*(.)	57.336	0.70	0.06647	0.7064	3	15.902
***φ*(.)*p*(.)**	57.348	0.71	0.06607	0.7022	2	18.137
φ(.)*p*(5T)	57.705	1.06	0.05526	0.5873	3	16.272
φ(.)*p*(T)	57.729	1.09	0.05460	0.5803	3	16.296
φ(2T)*p*(.)	57.805	1.16	0.05258	0.5588	3	16.371
φ(.)*p*(4T)	57.822	1.18	0.05213	0.5540	3	16.388
φ(.)*p*(3T)	57.823	1.18	0.05210	0.5537	3	16.390
φ(.)*p*(2T)	58.127	1.49	0.04475	0.4756	3	16.694
***φ*(t)*p*(t)§**	58.174	1.53	0.04228	0.4644	6	9.5622
φ(3T)*p*(2T)	58.855	2.21	0.03110	0.3305	4	15.117
φ(3T)*p*(3T)	58.931	2.29	0.02993	0.3181	4	15.193
φ(3T)*p*(5T)	58.935	2.29	0.02988	0.3176	4	15.197
φ(3T)*p*(T)	58.937	2.30	0.02985	0.3172	4	15.199
φ(3T)*p*(4T)	58.941	2.30	0.02979	0.3166	4	15.203
φ(T)*p*(T)	59.087	2.45	0.02770	0.2944	4	15.349
φ(4T)*p*(2T)	59.312	2.67	0.02474	0.2629	4	15.574
φ(4T)*p*(T)	59.346	2.70	0.02433	0.2586	4	15.608
φ(4T)*p*(3T)	59.361	2.72	0.02414	0.2566	4	15.623
φ(5T)*p*(2T)	59.484	2.84	0.02271	0.2414	4	15.746
φ(5T)*p*(T)	59.534	2.89	0.02214	0.2353	4	15.796
φ(5T)*p*(3T)	59.553	2.91	0.02194	0.2332	4	15.815
φ(5T)*p*(5T)	59.566	2.92	0.02180	0.2317	4	15.828

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 9. CJS models for black bears on Rowan Creek 2002. Only models with ΔAICc ≤ 3.0 and *φ*(t)*p*(t) are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (T) indicates a trend in the parameter over time, where (XT) refers to the number of groupings into which intervals were collapsed. (t) refers to a time-specific (non-linear) effect on the parameter, where (Xt) refers to two groupings of intervals. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
***φ*(.)*p*(.)**	207.641	0.00	0.12543	1.0000	2	71.148
φ(3t)*p*(.)	208.225	0.58	0.09369	0.7470	3	69.607
φ(.)*p*(3t)	209.251	1.61	0.05609	0.4472	4	68.463
φ(.)*p*(T)	209.264	1.62	0.05573	0.4443	3	70.645
φ(T)*p*(.)	209.299	1.66	0.05476	0.4366	3	70.681
φ(.)*p*(3T)	209.328	1.69	0.05396	0.4302	3	70.710
φ(.)*p*(6T)	209.361	1.72	0.05310	0.4234	3	70.742
φ(.)*p*(4T)	209.458	1.82	0.05056	0.4031	3	70.840
φ(.)*p*(2T)	209.495	1.85	0.04964	0.3958	3	70.877
φ(.)*p*(2t)	209.495	1.85	0.04964	0.3958	3	70.877
φ(3T)*p*(.)	209.526	1.88	0.04889	0.3898	3	70.907
φ(.)*p*(5T)	209.723	2.08	0.04430	0.3532	3	71.104
φ(.)*p*(2t)	209.734	2.09	0.04405	0.3512	3	71.116
***φ*(t)*p*(t)§**	227.172	19.5	0.00001	0.0001	13	64.617

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

Table A6 – 10. CJS models for black bears on Skinny Rowan Creek 2002. Only models with ΔAICc ≤ 3.0 and *φ*(.)*p*(.) are presented. **Bold** indicates the constant ***φ*(.)*p*(.)** and saturated ***φ*(t)*p*(t)** models. *φ*(t)*p*(t) was the most saturated model run as cohorts were pooled. (.) indicates that the parameter is constant over all time intervals. (t) refers to a time-specific (non-linear) effect on the parameter. (T) indicates a trend in the parameter over time, where (XT) refers to the number of groupings into which intervals were collapsed. *φ* represents apparent survival, or the likelihood of a bear remaining on the stream from one interval to the next, and *p* represents recapture probability.

Model	AICc	ΔAICc	AICc weight	Model likelihood	# Parameters	Deviance
φ(3T)*p*(.)	102.584	0.00	0.07618	1.0000	3	64.257
φ(5T)*p*(.)	103.059	0.48	0.06006	0.7884	3	64.733
φ(T)*p*(.)	103.238	0.65	0.05493	0.7210	3	64.911
φ(3T)*p*(6T)	103.530	0.95	0.04746	0.6230	4	62.789
φ(4T)*p*(.)	103.898	1.31	0.03948	0.5182	3	65.572
φ(6T)*p*(.)	103.979	1.40	0.03791	0.4976	3	65.652
φ(6T)*p*(T)	104.185	1.60	0.03421	0.4490	4	63.443
φ(3T)*p*(T)	104.323	1.74	0.03193	0.4191	4	63.582
φ(6T)*p*(6T)	104.391	1.81	0.03086	0.4051	4	63.650
φ(3T)*p*(4T)	104.477	1.89	0.02956	0.3880	4	63.735
φ(6T)*p*(4T)	104.512	1.93	0.02905	0.3813	4	63.771
φ(6T)*p*(2T)	104.515	1.93	0.02901	0.3808	4	63.773
φ(3T)*p*(2T)	104.529	1.95	0.02880	0.3780	4	63.788
φ(6T)*p*(5T)	104.572	1.99	0.02820	0.3702	4	63.830
φ(3T)*p*(5T)	104.672	2.09	0.02681	0.3519	4	63.931
φ(4T)*p*(6T)	104.864	2.28	0.02436	0.3198	4	64.122
φ(5T)*p*(T)	104.901	2.32	0.02392	0.3140	4	64.159
φ(6T)*p*(3T)	104.947	2.36	0.02338	0.3069	4	64.205
φ(T)*p*(T)	104.983	2.40	0.02295	0.3012	4	64.242
φ(3T)*p*(3T)	104.996	2.41	0.02280	0.2993	4	64.255
φ(5T)*p*(2T)	105.006	2.42	0.02269	0.2978	4	64.265
***φ*(t)*p*(t)§**	**105.257**	**2.67**	**0.01962**	**0.2627**	**8**	**53.515**
φ(5T)*p*(5T)	105.109	2.53	0.02155	0.2829	4	64.367
φ(5T)*p*(4T)	105.120	2.54	0.02143	0.2813	4	64.379
φ(T)*p*(2T)	105.136	2.55	0.02126	0.2791	4	64.395
φ(T)*p*(4T)	105.183	2.60	0.02077	0.2726	4	64.442
φ(T)*p*(6T)	105.255	2.67	0.02003	0.2629	4	64.514
φ(T)*p*(5T)	105.358	2.77	0.01903	0.2498	4	64.616
φ(5T)*p*(3T)	105.407	2.82	0.01857	0.2438	4	64.665
φ(T)*p*(3T)	105.603	3.02	0.01683	0.2209	4	64.862
***φ*(.)*p*(.)**	**107.094**	**4.51**	**0.00799**	**0.1049**	**2**	**71.066**

§ Information on relative fit of *φ*(t)*p*(t) if it were to be included in the set of models, however since many time-specific parameters were inestimable, this model was removed from the group, and therefore AICc weights presented for all other models do not incorporate the influence of the *φ*(t)*p*(t) model.

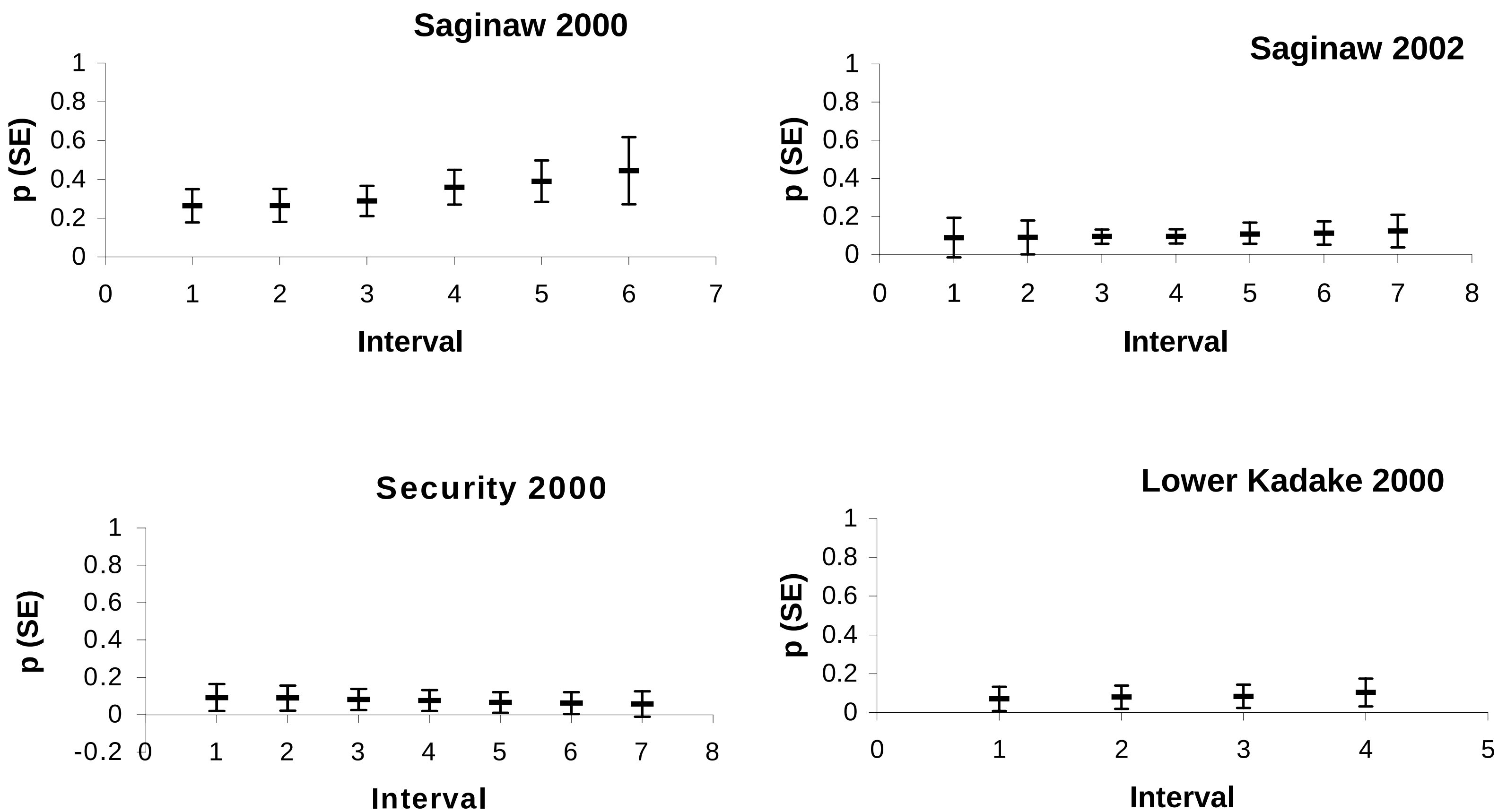
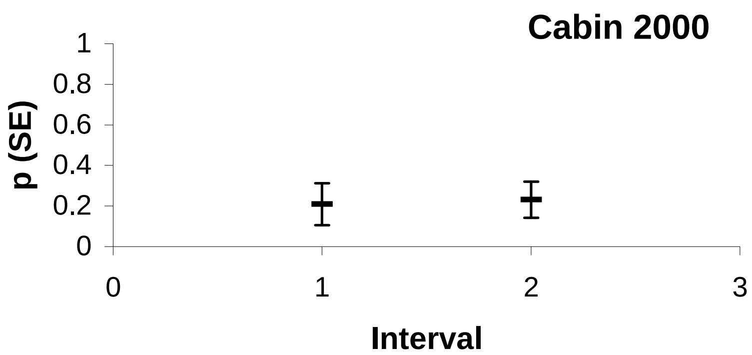
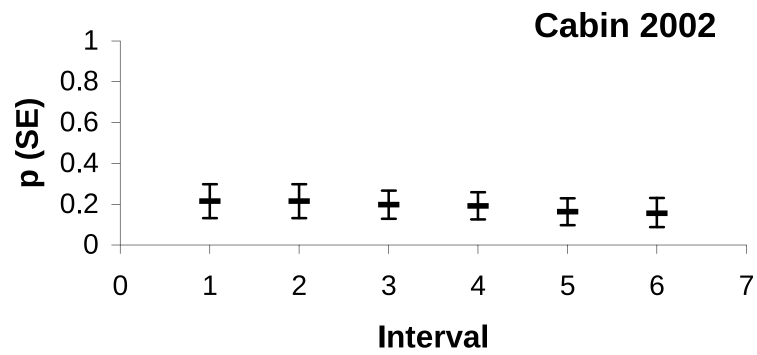
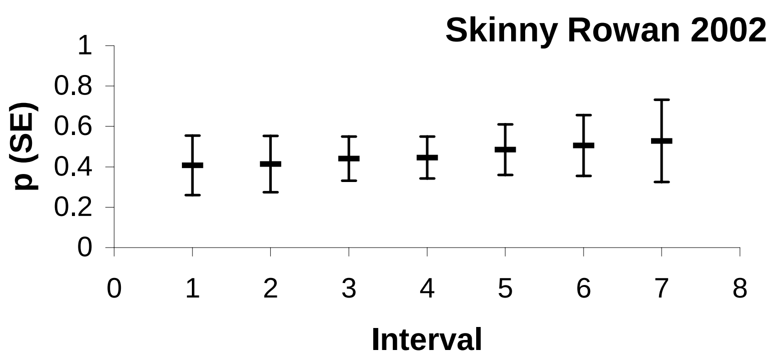
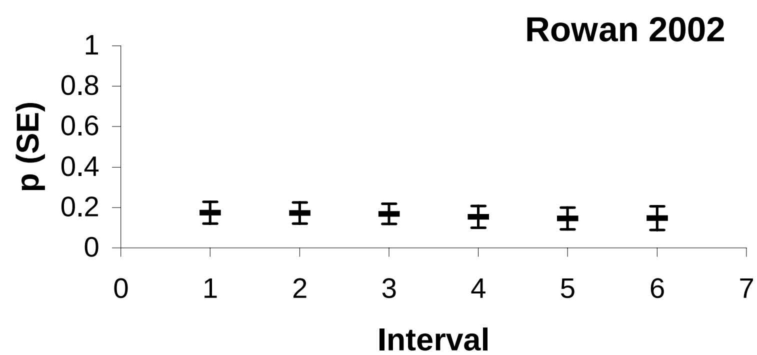


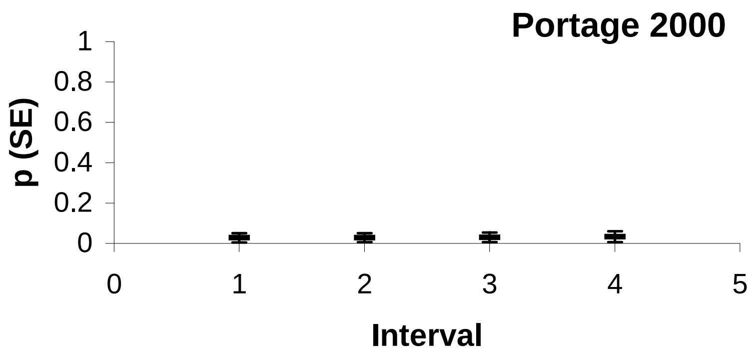
Figure A6 – 1. Recapture probabilities (p) for black bears in ten salmon stream-year data sets over week-long intervals, as estimated in CJS. All estimates are model-averaged. Error bars are ± SE.

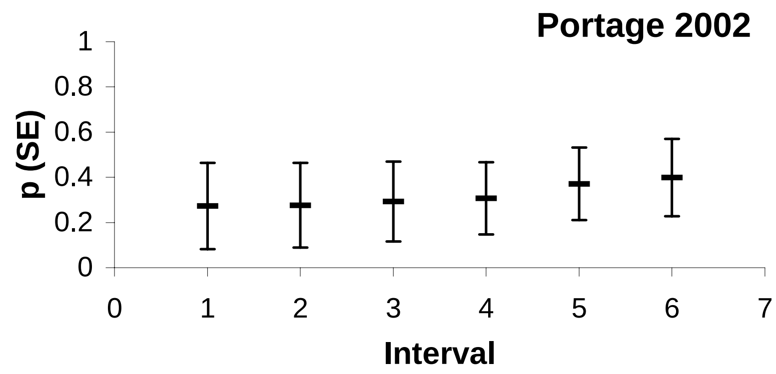

Cabin 2000
p (SE)
1
0.8
0.6
0.4
0.2
0
0
1
2
3
Interval


Cabin 2002
p (SE)
1
0.8
0.6
0.4
0.2
0
0
1
2
3
4
5
6
7
Interval


Skinny Rowan 2002
p (SE)
1
0.8
0.6
0.4
0.2
0
0
1
2
3
4
5
6
7
8
Interval


Rowan 2002
p (SE)
1
0.8
0.6
0.4
0.2
0
0
1
2
3
4
5
6
7
Interval


Portage 2000
p (SE)
1
0.8
0.6
0.4
0.2
0
0
1
2
3
4
5
Interval


Portage 2002
p (SE)
1
0.8
0.6
0.4
0.2
0
0
1
2
3
4
5
6
7
Interval

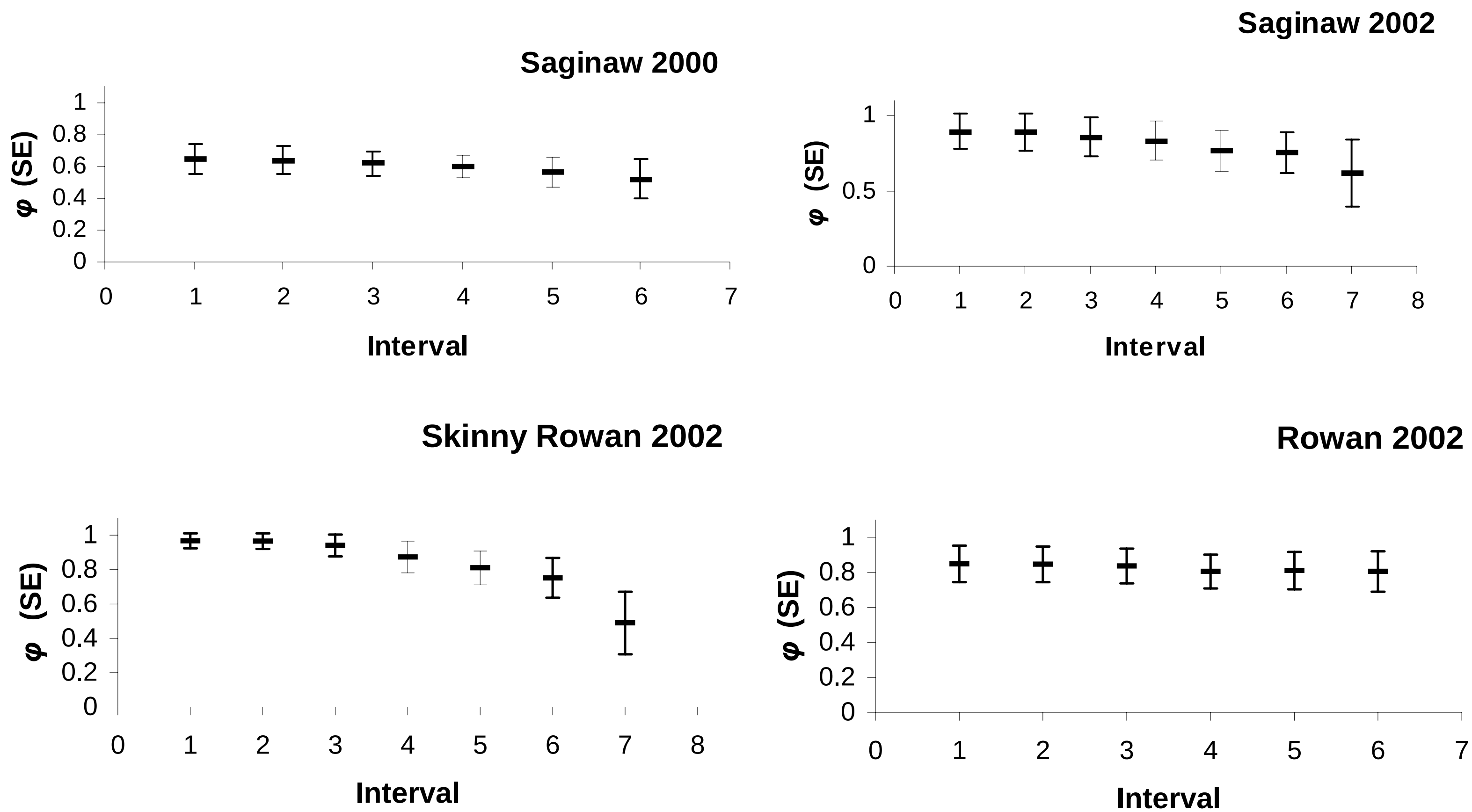
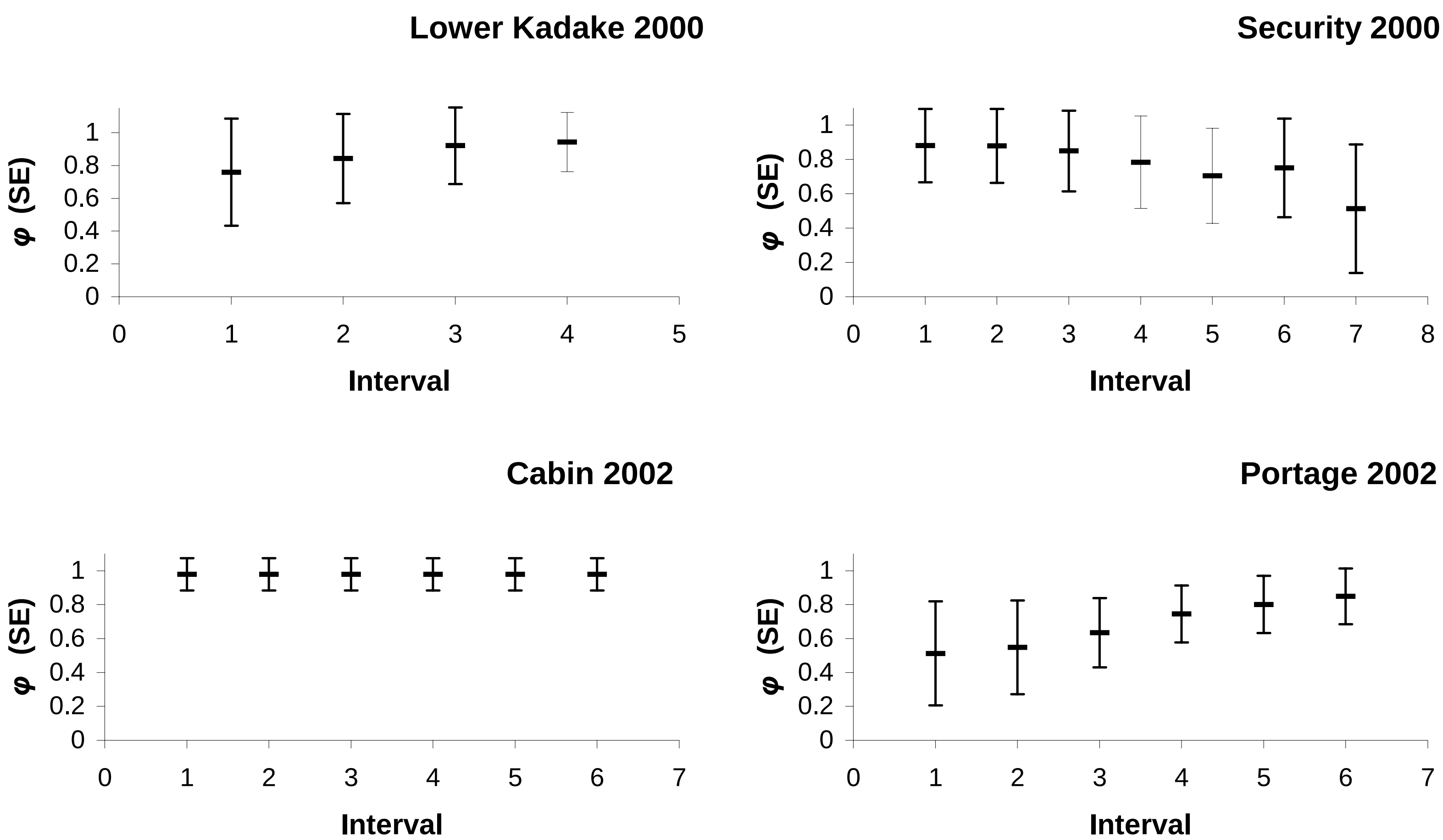


Figure A6 – 2. Apparent survival (φ), for black bears for eight salmon stream-year data sets over week-long intervals, as estimated in CJS. All φ are model-averaged estimates. Error bars are ± SE.


Lower Kadake 2000
Security 2000
Cabin 2002
Portage 2002
φ (SE)
Interval
0
0.2
0.4
0.6
0.8
1
0
1
2
3
4
5
6
7
8